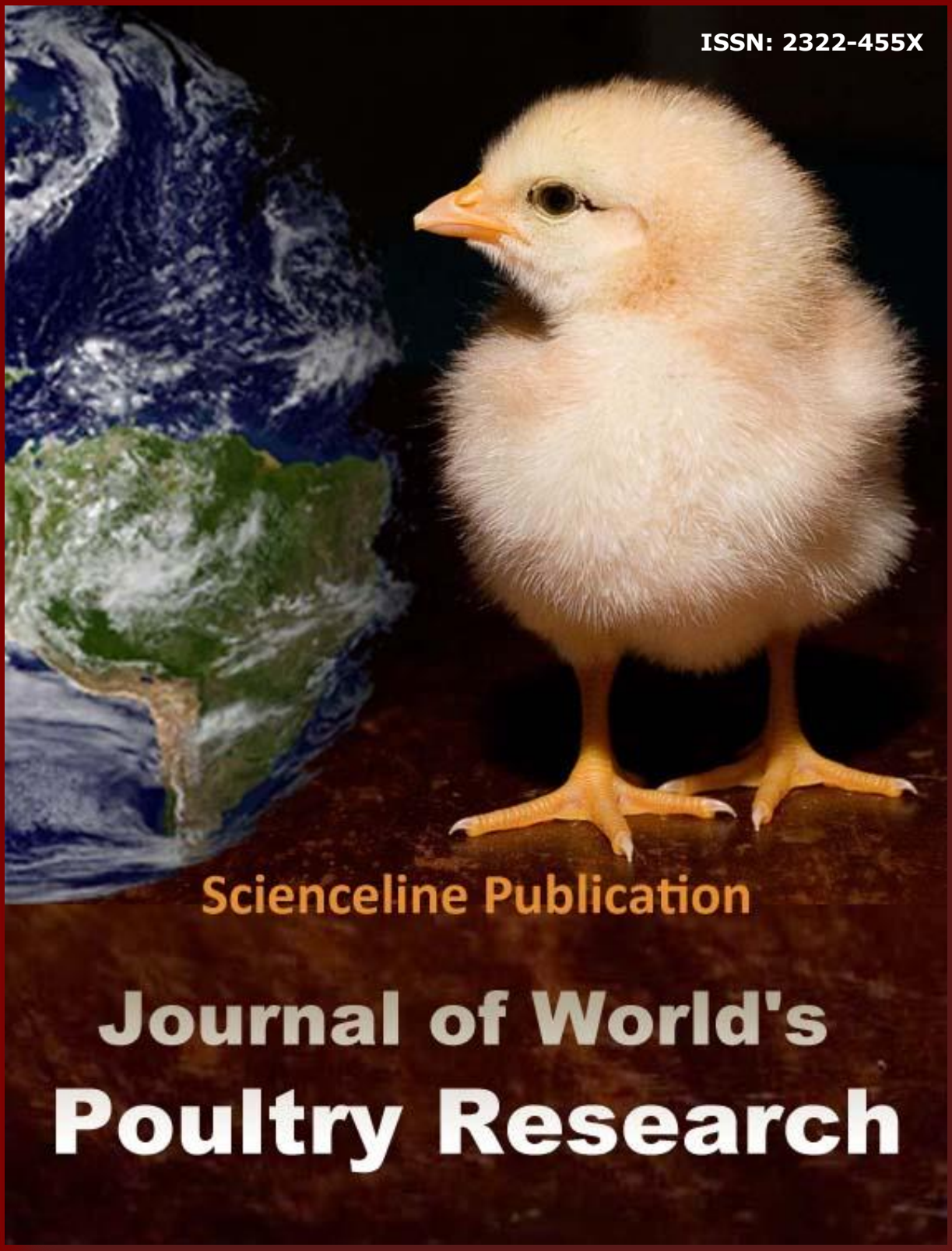
In the Name of God



An international peer-reviewed journal which publishes in electronic format

Volume 10, Issue 4, December 2020

Journal of World's Poultry Research

J. World Poult. Res. 10 (4): 545-661; December 25, 2020

Editorial Team

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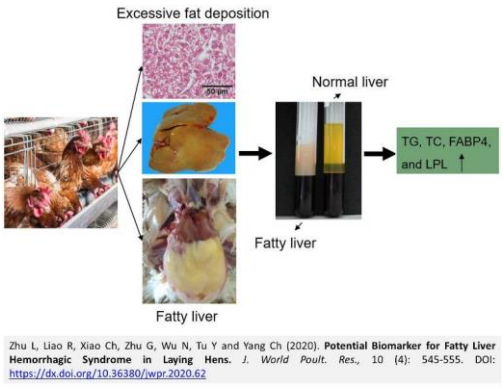
Volume 10 (4); December 25, 2020

Research Paper

Potential Biomarker for Fatty Liver Hemorrhagic Syndrome in Laying Hens.

Zhu L, Liao R, Xiao Ch, Zhu G, Wu N, Tu Y and Yang Ch.

J. World Poult. Res. 10(4): 545-555, 2020; pii: S2322455X2000062-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.62



Zhu L, Liao R, Xiao Ch, Zhu G, Wu N, Tu Y and Yang Ch (2020). **Potential Biomarker for Fatty Liver Hemorrhagic Syndrome in Laying Hens.** *J. World Poult. Res.*, 10 (4): 545-555. DOI: https://dx.doi.org/10.36380/jwpr.2020.62

ABSTRACT: Fatty liver hemorrhagic syndrome is more common in laying hens with excess body weight (BW) and in the middle and late phase of egg production. However, no specific biomarkers in chickens can be used to diagnose liver steatosis or liver injury. The present study aimed to assess whether BW can be used to predict fatty liver in aged laying hens. This study also searched for potential plasma FLHS biomarkers. For these purposes, correlation among BW, relative weight of liver and abdominal fat, and plasma markers were analyzed in Hy-line brown laying hens. Furthermore, plasma levels of potential biomarkers were analyzed during the formation of fatty liver. Concentrations of triglycerides and total cholesterol were positively associated with BW in aged laying hens, while liver fat deposition was similar among chickens with different BW, indicating that BW cannot be used as the only criterion to discriminate aged laying hens with liver steatosis. A trend of increasing triglyceride, total cholesterol, fatty acid-binding protein 4 (FABP4), and lipoprotein lipase levels was found as age increased, and they were positively associated with BW indicating that they might be risk markers for FLHS in laying hens. The findings indicated that the plasma level of FABP4 was positively associated with the severity of fatty liver in aged laying hens. All the above results suggested that FABP4 might be a potential diagnostic indicator for FLHS.
Key words: Biomarker, Egg production, Fatty liver, Laying hens, Poultry

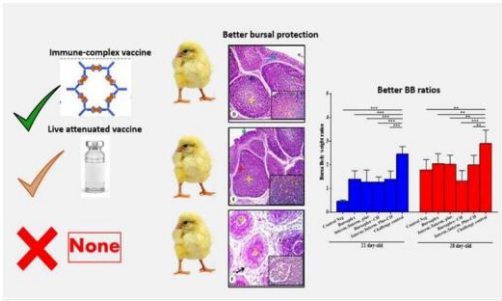
[Full text-PDF] [XML] [Crossref Metadata]

Research Paper

Immune-Complex Infectious Bursal Disease Virus versus Live Attenuated Vaccines to Protect SPF Chicken against Very Virulent Virus Challenge.

Abou El-Fetouh MS, Hafez MH, El-Attar ER and El-Agamy ME.

J. World Poult. Res. 10(4): 556-564, 2020; pii: S2322455X2000063-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.63



Abou El-Fetouh MS, Hafez MH, El-Attar ER and El-Agamy ME (2020). **Immune-Complex Infectious Bursal Disease Virus versus Live Attenuated Vaccines to Protect SPF Chicken against Very Virulent Virus Challenge.** *J. World Poult. Res.*, 10 (4): 556-564. DOI: https://dx.doi.org/10.36380/jwpr.2020.63

ABSTRACT: In this study infectious bursal disease (IBD) vaccinations were evaluated against very virulent IBD (vvIBDV) challenge and were compared. A total of 120-day-old white Leghorn SPF chickens were divided into 6 groups (each was 20 birds). Two groups were vaccinated on either day 1 with an immune-complex vaccine. The second groups were vaccinated at days 9 and 14 of age using intermediate and intermediate plus IBD vaccines, respectively the balance groups are controls. All vaccines were administered according to the manufacturer's instructions. The challenge was conducted on the 16 days of age using 105 EID50 /0.1 ml of a vvIBDV strain via the oculonasal route. The antibody immune response was monitored in all groups at 14, 21, 28, and 35 days of age. The performance, bursal gross lesions, challenge virus detection, and bursal histopathology were evaluated in vaccinated non challenged and vaccinated challenged birds at days 21 and 28 of age. All vaccinated groups were protected against the vvIBDV challenge compared to 40% mortality in the challenge control group. Both the immune-complex and live attenuated IBD vaccine groups showed similar bursa body weight (BB) ratios compared to the negative control group. The immune-complex vaccinated groups antibody titers were significantly higher except on 28th day of age. Upon challenge, the intermediate/intermediate plus vaccinated challenged group showed higher antibody titers at 21 and 35th with the challenge virus detection and quantification on day 28. The immune-complex vaccinated challenged group developed milder bursal histopathology signs but no differences between the 2 vaccine programs were seen. It can be understandable, the use of either immune-complex vaccine at day-old or early vaccination with intermediate followed by intermediate plus live attenuated IBD vaccines induced protective antibody titers and protect chickens against an early vvIBDV challenge. The suggested schedules need further evaluation in commercial broilers with maternal derived IBD antibodies to simulate field conditions.
Keywords: Immune-Complex vccine, Infectious Bursal Disease, Live Attenuated Vaccine, SPF Chicken

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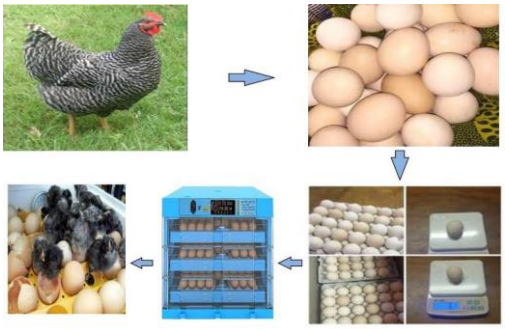
Research Paper

Reproductive Performance of Koekoek Chickens at Different Levels of Feed Restrictions.



Molapo Motsoene S, Webb E, Aloycia Mahlehla M, Chabeli Th, and Kompi P.

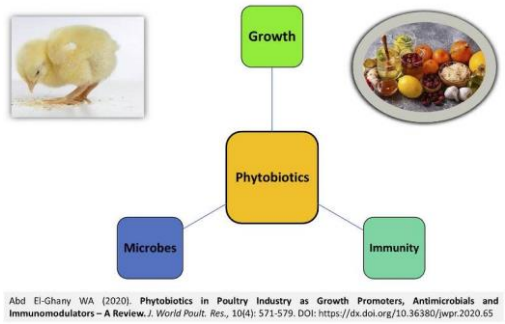
J. World Poult. Res. 10(4): 565-570, 2020; pii: S2322455X2000064-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.64

ABSTRACT: The objective of the present study was to determine the impact of the feeding levels on the reproductive characteristics of Koekoek chickens. A total of 270 Koekoek chickens were randomly assigned to 4 feeding level treatments in a completely randomized design. The four feeding level treatments were fully fed during the rearing and laying phase (AA), fully fed during the rearing phase and restricted feeding during the laying phase (AR), restricted feeding during the rearing phase and fully fed during the laying phase (RA), and restricted both during the rearing and laying phase (RR). The General Linear Model procedure (SPSS software, version 17) was used to analyze the data set. The pubic bone measurements were 23.6, 25.1, 16.1, and 15.1 mm for chickens that received AA, AR, RA, and RR treatments, respectively, at 18 weeks of age. At 32 weeks of age, chickens given AA and RA treatments had wider pubic bones than chickens given AR and RR treatments. Combined ova and oviduct weights were higher in the fully fed chickens at 18 weeks of age. Koekoek chickens in AA treatment had the highest average egg production. Chickens given AR treatment had lower average egg weights than those given AA, AR, and RR treatments. Chickens treated with AA and AR reached puberty earlier than those that were treated with the RA and RR treatments. The eggs produced by chickens given RR treatment had a higher average hatching percentage. The lowest percentage of hatches was observed in chickens that were fed ad libitum during the rearing phase. In conclusion, the feed restriction only during the rearing phase improved the reproduction performance of Koekoek chickens.
Keywords: Egg weight, Fully fed, Hatchability, Koekoek, Laying percentage, Oviduct, Pubic bone, Restricted

[Full text-PDF] [XML] [Crossref Metadata]

Review

Phytobiotics in Poultry Industry as Growth Promoters, Antimicrobials and Immunomodulators – A Review.



Abd El-Ghany WA.
J. World Poult. Res. 10(4): 571-579, 2020; pii: S2322455X2000065-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.65

ABSTRACT: Due to the hazardous use of antimicrobials in poultry production sector, development of drug resistance have become a worldwide problem. Therefore, using biotic or natural products, such as phytobiotics (phytogenics or botanicals) have received a great attention as antibiotic substitutes. The use of phytobiotics or their constituents have been considered as a relatively new class of natural herbs that gained popularity and acceptability among poultry farmers. The incorporation of several types of phytobiotic additives in poultry feed have proved their ability to enhance the productive performance of broilers as well as layers. Moreover, phytbiotics presented great efficacy in counteracting intestinal pathogenic microorganism while maintaining the population of normal inhabitant beneficial microflora. Immunostimulatory effect on both humoral and cellular immunity as well as antioxidant properties were recorded as characters of phytobiotics. Therefore, this review article aimed to give a spotlight on the uses of different types of phytobiotics as poultry dietary additives to improve the productive parameters, reduce the pathogenic intestinal bacteria, and potentiate the immune response, especially after vaccination processes.
Keywords: Antimicrobial, Immunity, Performance, Plants, Poultry

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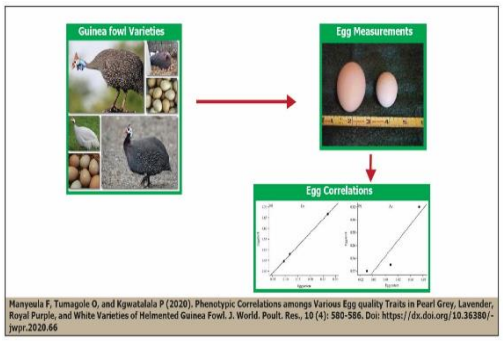
Research Paper

Phenotypic Correlations among Various Egg Quality Traits in Pearl Grey, Lavender, Royal Purple, and White Varieties of Helmeted Guinea Fowl.



Manyeula F, Tumagole O and Kgwatalala P.

J. World Poult. Res. 10(4): 580-586, 2020; pii: S2322455X2000066-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.66

ABSTRACT: Guinea fowls are increasingly popular in Botswana since

they not only provide an alternative to access protein in the form of eggs and meat but also become a good source of income for the peasants. There are different varieties of Guinea fowl in Botswana, including pearl grey, lavender, royal purple, and white. Indeed, there is a need to conduct more studies related to the phenotypic correlations among egg quality traits in different varieties of helmeted guinea fowl found in Botswana. Therefore, the present study was targeted toward the evaluation of both the external and internal quality characteristics of the four different varieties of the domesticated helmeted guinea fowl found in Botswana. In this regard, a total of 150 eggs were collected from the so-called varieties of domesticated helmeted guinea fowl. The egg weight was positively and significantly correlated with egg length, egg width, shell weight, egg surface area, and egg volume; however, the egg weight was negatively correlated with egg shape index. Of the four varieties of domesticated helmeted guinea fowl found in Botswana, the white variety had the strongest correlation coefficients with various external egg quality traits and different internal egg quality characteristics. The lavender variety had the highest correlation coefficients with internal and external egg quality traits. It seems that the selection for higher egg weight as is the case in the current egg grading system can lead to the greatest improvements in other egg quality characteristics in the white and lavender varieties, compared to the pearl grey and royal purple varieties. Therefore, the lavender and white varieties are the potential candidates for the possible selection of layer-type guinea fowl varieties.
Keywords: Botswana, Egg traits, Guinea fowl, Layer-type

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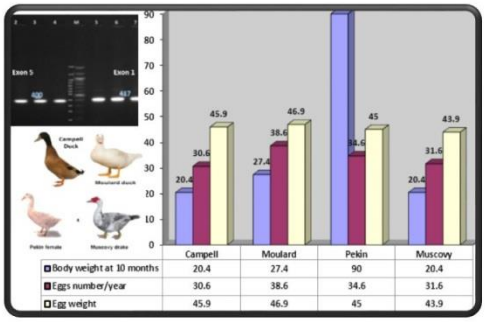
Research Paper

Polymorphism of the Prolactin Gene in Egyptian Duck Breeds.



Sabry NM, Mabrouk DM, Abdelhafez MA, El-Komy EM and Mahrous KF.

J. World Poult. Res. 10(4): 587-598, 2020; pii: S2322455X2000067-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.67

ABSTRACT: In avian, the prolactin hormone triggers and regulates ovarian follicle development. This study aims to detect the Prolactin (*PRL*) gene polymorphisms (exons 1and5) in four Egyptian duck breeds, namely Campbell, Moulard, Muscovy, and Pekin using PCR-RFLP technique and sequence analysis. It also investigated the association of this gene with egg production, egg weight, and body weight. The present results revealed that *PRL* gene exon 1 and part of intron 1 showed two alleles A and B (polymorphic) in each of Campbell and Moulard, however, Muscovy and Pekin had only one allele (monomorphic). The allele A was more dominant with frequencies of 0.70, 0.60, and 1.00, compared to the allele B (0.30, 0.40, and 0.00) for Campbell, Moulard, and Muscovy, respectively. For Pekin, the allele B only appeared with the frequency of 1.0. Ducks with the high frequency of allele A were superior at egg weight, compared to others. Furthermore, for *PRL* gene exon 5, there were two alleles G and C (polymorphic) in Campbell, Moulard, and Muscovy, however, Pekin had only one allele (monomorphic). The allele G was more dominant (0.15, 0.74, 0.0, and 0.84) than the allele C (0.85, 0.26, 1.0, and 0.15) for Campbell, Moulard, Pekin, and Muscovy, respectively. Ducks having a high frequency of allele C were superior at egg production. Furthermore, there were many single nucleotide polymorphisms (SNPs) in the sequences in all breeds. The utmost ones exist at the restriction sites of *Xba*I enzyme for the amplified fragment, in the promotor, exon 1 and intron 1 (T378C in intron 1), and *Dra*I enzyme for that in exon 5 (A5871G in exon 5).
Keywords: Duck, Genetic polymorphism, Genotyping, Prolactin gene

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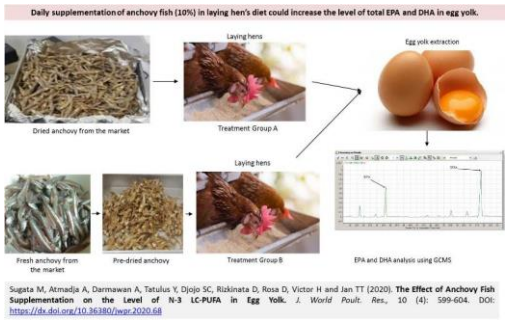
Research Paper

The Effect of Anchovy Fish Supplementation on the Level of N-3 LC-PUFA in Egg Yolk.



Sugata M, Atmadja A, Darmawan A, Tatulus Y, Djojo SC, Rizkinata D, Rosa D, Victor H and Jan TT.

J. World Poult. Res. 10(4): 599-604, 2020; pii: S2322455X2000068-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.68

ABSTRACT: Since the recommended daily intake of n-3 LC-PUFA is rarely met, interest in food enrichment has been increasing. It is known that dietary supplementation could alter the level and type of PUFA in the egg. Hence, the present study focused on the enrichment of egg yolk by the addition of 10% anchovy fish to the chicken diet. Based on gas chromatography analysis, dried and pre-dried anchovy from Indonesia contained a considerable amount of total eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), which was 60.10 g and 68.80 mg/100 g, respectively. After 24 days of anchovy supplementation, DHA-rich anchovy fish oil diet caused a significant increase of DHA but not EPA in egg yolk. Hens fed with anchovy could produce eggs with a higher amount of total EPA and DHA, which was up to 155.98-201.53%, as compared to control eggs. Furthermore, the sensory profile of control and enriched eggs was also evaluated. There was no significant difference in texture, aroma, flavor, and appearance between control and enriched eggs. In conclusion, this study indicated that anchovy fish supplementation could increase the level of EPA and DHA in egg yolk without causing any sensory changes in the yolk.
Keywords: Anchovy, DHA, Egg yolk, Enrichment, EPA
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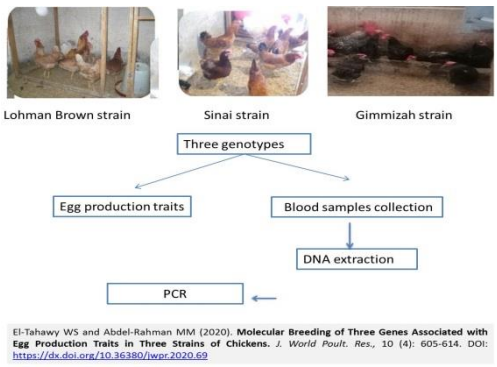
Research Paper

Molecular Breeding of Three Genes Associated with Egg Production Traits in Three Strains of Chickens.



El-Tahawy WS and Abdel-Rahman MM (2020). **Molecular Breeding of Three Genes Associated with Egg Production Traits in Three Strains of Chickens.** *J. World Poult. Res.*, 10 (4): 605-614. DOI: https://dx.doi.org/10.36380/jwpr.2020.69

El-Tahawy WS and Abdel-Rahman MM.

J. World Poult. Res. 10(4): 605-614, 2020; pii: S2322455X2000069-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.69

ABSTRACT: Breeding programs play an important role in increasing the performance of chickens. The poultry industry regards growth and reproduction as the two most economically valued characteristics for providing adequate animal proteins. Genetic variations are the basis of animal breeding. The present study was conducted on three genes, including Prolactin, 3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase (HMGCR), and Gonadotropin-Releasing Hormone Receptor (GNRHR). DNA was isolated from 48 chickens taken from three strains Lohmann Brown (17), Sinai (24), and Gimmizah (7) for Prolactin, HMGCR, and GNRHR gene amplification by using the PCR protocol. Electrophoresis was performed on the PCR products and the bands were viewed on a transilluminator. The size of the Prolactin gene, HMGCR, and GNRHR were 154, 675, and 210 bp, respectively. For the Sinai strain, five bands for Prolactin, two bands for HMGCR, and six bands for GNRHR were found while for the Lohmann Brown strain, five bands of Prolactin gene, three bands for HMGCR, and five bands for GNRHR were found. Regarding the Gimizah strain, two bands were found for Prolactin and GNRHR genes and there was only one band for the HMGCR gene. The Lohmann Brown strain respectively matured 13 and 91 earlier than Gimizah and Sinai strains with a higher egg number during the first 90 days.
Keywords: Breeding, Chickens, Egg production, GNRHR gene, HMGCR gene, Prolactin gene, PCR

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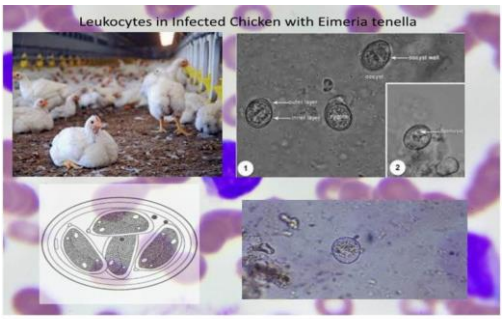
Research Paper

The Effect of Dietary Administration of Virgin Coconut oil on Differential Leukocytes in Infected Chicken with Eimeria tenella.



Faradilla ZSh, Yunus M and Hermadi HA (2020). **The Effect of Dietary Administration of Virgin Coconut oil on Differential Leukocytes in Infected Chicken with *Eimeria tenella*.** *J. World Poult. Res.*, 10 (4): 615-622. DOI: https://dx.doi.org/10.36380/jwpr.2020.70

Faradilla ZSh, Yunus M and Hermadi HA.
J. World Poult. Res. 10(4): 615-622, 2020; pii: S2322455X2000070-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.70

ABSTRACT: Coccidiosis is the main problem in poultry diseases. It is caused by the parasite *Eimeria tenella,* which induce the immune response of leukocyte. Anticoccidial drugs are administered in the poultry feed to control coccidiosis. However, taking medication for a long time can lead to resistance. Recent studies have indicated that Virgin Coconut Oil (VCO) has some benefits, including anti-inflammatory effects. The present research aimed to identify the effect of VCO at the different doses in improving the various leukocyte counts of chickens infected with *E. tenella*. Male chickens were divided into five groups (T0, T1, T2, T3, and T4) and treated for 28 days. T0 was neither infected with *E. tenella* nor get treatment, T1 was only infected with *E. tenella*, T2 was treated with 5 ml/kg VCO feed and had *E. tenella* infection, T3 was treated with 10 ml/kg VCO feed and had *E. tenella* infection, and T4 was treated 20ml/kg VCO feed and had *E. tenella* infection. Differential leukocyte was counted with a blood cell counter. The data obtained were analyzed using ANOVA and Duncan's Multiple Range Test. The results indicated that a dose of 10 ml/kg feed and 20ml/kg feed of VCO could improve the differential leukocyte counts of chickens infected with *E. tenella* by maintaining the counts of basophil, eosinophil, heterophil, monocyte, and lymphocyte in the normal range. The present study concluded that VCO by a dose of more than 10 ml/kg would improve the differential leukocyte counts of chickens infected with *E. tenella*.
Keywords: Differential leukocyte count, *Eimeria tenella*, Virgin Coconut Oil

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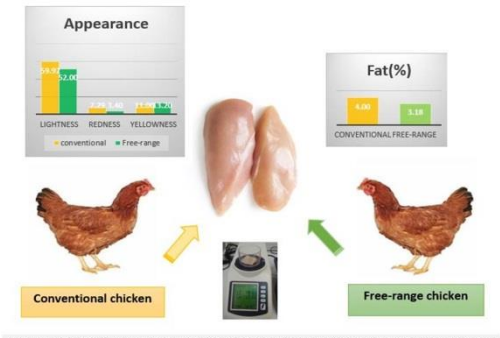
Research Paper

Characteristics of Carcass Traits and Meat Quality of Broiler Chickens Reared under Conventional and Free-range Systems.



Davoodi P and Ehsani A (2020). **Characteristics of Carcass Traits and Meat Quality of Broiler Chickens Reared under Conventional and Free-range Systems.** *J. World Poult. Res.*, 10 (4): 623-630. DOI: https://dx.doi.org/10.36380/jwpr.2020.71

Davoodi P and Ehsani A.

J. World Poult. Res. 10(4): 623-630, 2020; pii: S2322455X2000071-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.71

ABSTRACT: Alternative chicken production systems have become popular in recent years due to animal welfare criteria and consumer's

perceptions. General beliefs express that the meat quality of chicken reared under free-range systems is better than that of chickens under conventional production conditions. The aim of this study was to compare the meat quality and carcass traits of chickens raised in conventional and free-range systems. Either conventional or free-range systems used meat-type Hubbard JA57 birds with a slaughter age of approximately 78 days. For assessing carcass traits and meat quality, six male chickens were selected from each system. The meat quality parameters, pH at 45 minutes, ultimate pH, color coordinates, drip loss, cooking loss, and water-holding capacity were measured. Furthermore, proximate parameters, such as crude protein, total fat, and crude ash were determined. There were no significant differences in main carcass yield and breast muscles between chickens reared in two systems, however, color values dramatically were influenced by rearing systems. Breast muscle samples from birds reared under the conventional system had a smaller hue angle and saturation value than those from the free-range birds. Moreover, the drip loss parameter was significantly higher in free-range chickens. The ash and protein contents of breast muscles were similar although raw breast meat from free-range birds had significantly lower fat content. The results prove that a free-range rearing system can modify the appearance, color values, and fat content of chicken meat and it can be a part of the interests of meat production consumers.
Keywords: Broiler chickens, Free-range, Hubbard JA57, Intensive rearing system, Meat quality

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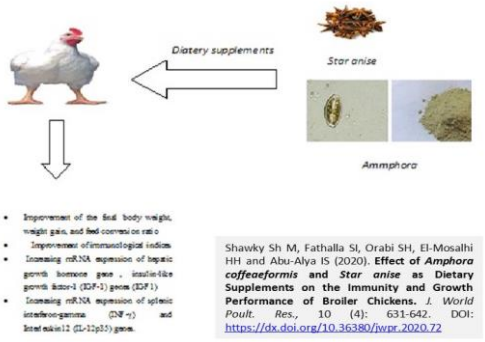
Research Paper

Effect of *Amphora coffeaeformis* and *Star anise* as Dietary Supplements on the Immunity and Growth Performance of Broiler Chickens.



Shawky Sh M, Fathalla SI, Orabi SH, El-Mosalhi HH and Abu-Alya IS.

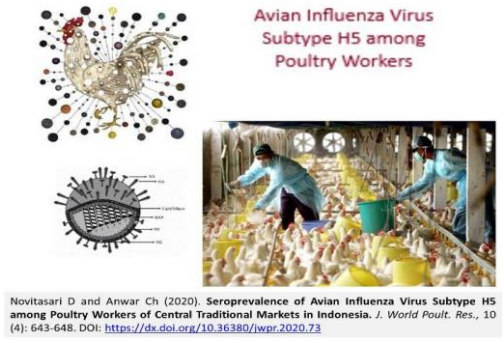
J. World Poult. Res. 10(4): 631-642, 2020; pii: S2322455X2000072-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.72

ABSTRACT: The present study was designed to evaluate the impacts of daily dietssupplemented with *Amphora coffeaeformis* and *Star anise* on growth performance and immunity of Cobb broiler chickens. *Amphora coffeaeformis* is considered a potent free radical scavenger due to the presence of β-carotene and fucoxanthin, which are used widely as food additives. *Star Anise* has a natural antioxidant, which can also be used for the chemo-prevention of disease occurring due to oxidative deterioration. A total of 270 broiler chickens were divided into three groups, each with three replicates of 30 birds. The control group (G1) was given the basal diet, the *Amphora* group (G2) received *Amphora* in a dose of 1g/Kg in the ration, and the *Star anise* group (G3) received *Star anise* in a dose of 2g /Kg in the ration. The results indicated that *Amphora* and *Star anise* significantly improved the final body weight, weight gain, and feed conversion ratio, total white blood cells count, phagocytic activity percentage, phagocytosis index in plasma, IgM, IgG, and A/G ratio in serum. In addition, *Amphora* and *Star anise* significantly increased mRNA expression of hepatic growth hormone gene, insulin-like growth factor-1 (IGF-1) genes (IGF1), and mRNA expression of splenic interferon-gamma (INF-γ) and Interleukin 12 (IL-12p35) genes from broiler chickens, compared to the control group. In conclusion, the use of fed additives, such as *Amphora coffeaeformis*and *Star anise* in the diet of broiler chickens for 35 days was sufficient to improve broiler growth performance and could modulate their immunity.
Keywords: *Amorphacoffeaeformis*, Broiler chickens, Diet supplementation, Growth performance, Immunity, *Star anise*

[Full text-PDF] [XML] [Crossref Metadata]

Research Paper

Seroprevalence of Avian Influenza Virus Subtype H5 among Poultry Workers of Central Traditional Markets in Indonesia.



Novitasari D and Anwar Ch.

J. World Poult. Res. 10(4): 643-648, 2020; pii: S2322455X2000073-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.73

ABSTRACT: Avian Influenza (AI) has been spread rapidly in almost all the provinces of Indonesia by the end of 2007, and it has become endemic. Avian Influenza viruses can be infecting to human from direct or indirect contact with the infected or dead poultry, and a visit to the wet poultry market in the neighborhood. Seroprevalence studies can be used to identify the clinical key, epidemiological studies, and the spread of AI viruses in humans. The aim of present study was to investigate the seroprevalence of Avian Influenza (AI) virus, subtype H5 among poultry workers at the central traditional market in industrial. To meet the mentioned demand, 26 blood samples were collected from the poultry workers via the median cubital vein. The antibody titer was examined using Hemagglutination Inhibition (HI) assay using H5 antigen from duck licensed under A/Dk/Indonesia/AU-78/12 (H5N1) and three kinds of red blood cells taken from horse, chicken and guinea pig. The serum samples were added with Receptor Destroying Enzyme (RDE) with a ratio of 3:1 (v/v) for an overnight, and pretreated with 10% of red blood cells before the HI assay was conducted. Based on the findings, it can be concluded that the percentage of seroprevalence of Avian Influenza (AI) virus, subtype H5 among poultry workers at central traditional market was 0%. Thirteen samples showed a negative result of the HI test. All of the workers' blood serum obtained less than 24 antibody titer from the HI test. As the results showed, the research on the poultry workers in the traditional market was carried out, and it obtained negative results; all the workers were not infected with the Avian

Influenza virus. In other words, Avian Influenza is not meaningful in poultry farm workers in Sidoarjo suburb traditional farms.
Keywords: Avian Influenza, Poultry workers, Seroprevalence, Traditional market.

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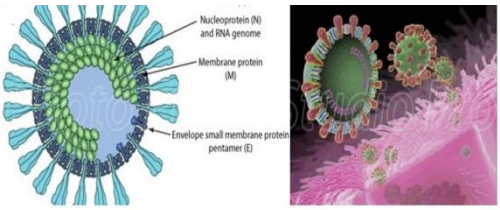
Research Paper

Characterization and Analysis of the Major Structural Protein Genes of the Recently Isolated Avian Infectious Bronchitis Virus in Egypt.

Yehia N, Said D and Zanaty AM.

J. World Poult. Res. 10(4): 649-661, 2020; pii: S2322455X2000074-10
DOI: https://dx.doi.org/10.36380/jwpr.2020.74



Yehia N, Said D and Zanaty AM (2020). **Characterization and Analysis of the Major Structural Protein Genes of the Recently Isolated Avian Infectious Bronchitis Virus in Egypt.** *J. World Poult. Res.*, 10 (4): 649-661. DOI: https://dx.doi.org/10.36380/jwpr.2020.74

ABSTRACT: Infectious Bronchitis Virus (IBV) is a severe infectious disease affecting chickens and causing serious economic loss. Although several studies have been conducted to characterize HVRs-S1 (Hyper-Variable Regions of Spike 1 gene) in Egypt, few of which aimed to characterize the major structural protein genes. In the present study, the genetic characterization of the major structural protein genes was carried out in 10 isolates selected from six governorates in 2019. Phylogenetically, the S1 gene was clustered into genotype GI-23 (variant II), with seven viruses that were clustered into Egy/Var II occurring in two subgroups (I, II) when aligned with previously isolated Egyptian strains. It had a specific character of 40 Amino Acids (AA) mutations except for IBV/EG/CV32/2019, which had 50 AA mutations, specifically in HVRs regions (HVRI, II, and III). The other three strains were clustered into Egy Var I with 17 AA mutations except IBV/EG/F859/ 2019, which had 15 AA mutations, compared to IBV/CU/4/2014 reference strain. The examined isolates had an additional glycosylation site at position 280 and one was missing at position 139 with the exception of two strains that only had an additional one, compared to IBV/CU/4/2014. The viruses in this study differed genetically from various vaccine seeds in the range of 69-83%. The Nucleocapsid, genetically characterized in the group of variant II (Egy/Var II) and the glycoprotein membrane genes genetically characterized in the variant group in a new sub-group with 11 and 9 AA mutations, respectively. The recombination event was only detected in the S1 gene in two isolates of IBV/EG/CV32/2019 and IBV/EG/F859/2019 from D274 and QX, respectively. In this regard, it is important to conduct continuous surveillance, pathogenicity study, and vaccine efficacy evaluation.
Keywords: Characterization, Infectious bronchitis virus, Major structure protein, Matrix, Nucleoprotein, Spike

[Full text-PDF] [XML] [Crossref Metadata]

Archive

Journal of World's Poultry Research

ISSN: 2322-455X

Frequency: Quarterly

Current Issue: 2020, Vol: 10, Issue: 4 (December 25)

Publisher: SCIENCELINE

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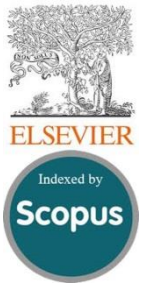

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Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 545-555, December 25, 2020

Research Paper, PII: S2322455X2000062-10

DOI: https://dx.doi.org/10.36380/jwpr.2020.62

Potential Biomarker for Fatty Liver Hemorrhagic Syndrome in Laying Hens

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Received: 09 Oct. 2020
Accepted: 20 Dec. 2020

ABSTRACT

Fatty liver hemorrhagic syndrome is more common in laying hens with excess body weight (BW) and in the middle and late phase of egg production. However, no specific biomarkers in chickens can be used to diagnose liver steatosis or liver injury. The present study aimed to assess whether BW can be used to predict fatty liver in aged laying hens. This study also searched for potential plasma FLHS biomarkers. For these purposes, correlation among BW, relative weight of liver and abdominal fat, and plasma markers were analyzed in Hy-line brown laying hens. Furthermore, plasma levels of potential biomarkers were analyzed during the formation of fatty liver. Concentrations of triglycerides and total cholesterol were positively associated with BW in aged laying hens, while liver fat deposition was similar among chickens with different BW, indicating that BW cannot be used as the only criterion to discriminate aged laying hens with liver steatosis. A trend of increasing triglyceride, total cholesterol, fatty acid-binding protein 4 (FABP4), and lipoprotein lipase levels was found as age increased, and they were positively associated with BW indicating that they might be risk markers for FLHS in laying hens. The findings indicated that the plasma level of FABP4 was positively associated with the severity of fatty liver in aged laying hens. All the above results suggested that FABP4 might be a potential diagnostic indicator for FLHS.

Key words: Biomarker, Egg production, Fatty liver, Laying hens, Poultry

INTRODUCTION

Similar to nonalcoholic fatty liver disease (NAFLD), fatty liver hemorrhagic syndrome (FLHS) is related to liver degeneration resulted from excessive fat deposition in the liver causing liver rupture, hemorrhage, and sudden death of chickens (Wolford and Polin, 1974; Whitehead 1979). Excessive fat deposition is also observed in the abdominal cavity. This disease mainly occurs in commercial caged laying hens leading to reduced egg production and death, and accordingly significant economic losses (Julian, 2005). Nowadays, FLHS is the most common noninfectious cause of high mortality in laying hens (Trott et al., 2014). It is currently believed that nutrition, genetics, and environmental toxins are related to FLHS outbreaks in laying hen farms, and the low-protein and high-energy diet is the main reason for the occurrence of FLHS (Diaz et al., 1999; Choi et al., 2012; Rozenboim et al., 2016). There are no obvious symptoms in the early stage of the disease, and the diagnosis can only be confirmed by dissecting the chickens with sudden onset. Therefore, screening of specific biomarkers for liver steatosis or liver damage would help improve the quality and efficiency of large-scale farmed laying hens.

Conventionally, FLHS is more prevalent in birds with excess body weight (BW) and in the middle and late phases of egg production. However, the idea of whether BW can be used as a marker for FLHS has remained to be verified. Additionally, in birds, the liver is the major organ of lipid metabolism, and steady changes in liver lipid metabolism are the basis of various forms of fatty liver disease. Excess fatty acid supply or inhibited oxidation in the liver may result in enhanced synthesis of triglycerides (TG) and disordered very low-density lipoprotein (VLDL) synthesis and secretion, which are observed in laying hens with FLHS (Dong and Tong, 2019; Gao et al., 2019). Circulating alanine aminotransferase (ALT) and aspartate aminotransferase (AST) are used as liver injury indicators and have been found to be increased in laying hens with

To cite this paper: Zhu L, Liao R, Xiao Ch, Zhu G, Wu N, Tu Y and Yang Ch (2020). Potential Biomarker for Fatty Liver Hemorrhagic Syndrome in Laying Hens. *J. World Poult. Res.*, 10 (4): 545-555. DOI: https://dx.doi.org/10.36380/jwpr.2020.62

FLHS (Hamid et al., 2019). Furthermore, many proteins in the blood, including those related to lipid metabolism, are synthesized in the liver, and the abundance and structure of these proteins also change in the development of liver disease, making them potential biomarkers for liver diseases including NAFLD (Kim et al., 2011; Vilar-Gomez and Chalasani, 2018). However, the clinical utility of these biomarkers has not been validated in chicken cohorts. The objectives of this study were, first, to assess whether BW can be used as an indicator for predicting fatty liver disease, and second, to screen potential plasma FLHS biomarkers in chickens.

MATERIALS AND METHODS

Ethical approval

All animal protocols used in this study were approved by the Ethics and Animal Welfare Committee of Shanghai Academy of Agricultural Sciences, China, and performed according to the guidelines established by 'the instructive notions with respect to caring for laboratory animals' issued by the Ministry of Science and Technology of the People's Republic of China (No. [2006] 398).

Animals and study design

A total number of 102,000 commercial Hy-line brown laying hens (20 to 65 weeks old) were raised in eight-high modular manure belt cages (Chore-Time Equipment Inc., Milford, IN, USA), with nine chickens per cage (dimensions of 60 × 65 × 45.5 cm) under standard commercial conditions. A standard commercial corn-soy diet (Shanghai Haifeng Dafeng Poultry Co. Ltd. Dafeng, Jiangsu, China) containing 16.00% crude protein, 0.73% lysine, 0.33% methionine, 4.1% calcium, 0.36% phosphorus, 0.17% salt, 19.3 ppm copper, 66 ppm iron, 80 ppm manganese, 0.3 ppm selenium, 2.2 ppm iodine, 80 ppm zinc, and 2700 kcal/kg calculated metabolizable energy was supplied for the layers. Feed and water were offered *ad libitum* throughout the experimental period. Separate groups of chickens were used for each experiment (Experiments 1-3).

Experiment 1

To verify whether BW can be used as a potential predictor of FLHS in aged laying hens, 60 laying hens aged 52 weeks were randomly divided into 4 groups according to the BW recommended by the Hy-line brown laying hens management guide (http://www.hy-line.co.uk/services/management-guides/). These four groups included low-grade weight (LW, 5% below standard weight), normal weight (NW, in standard weight range), overweight/obese (OW/Ob, <5% over standard weight), and seriously overweight/obese (SW/Ob, 5–10% over standard weight). The standard BW of Hy-line brown laying hens at 52 weeks should be 1.89 to 2.01 kg. To determine plasma concentrations of ALT, AST, TG, total cholesterol (TC), VLDL cholesterol (VLDL-C), fatty acid-binding protein 4 (FABP4), and lipoprotein lipase (LPL) blood samples from the experimental layers were obtained through the wing vein and collected in tubes containing EDTA as an anticoagulant. About 4 hours later, all the hens were killed by electric shock, and the abdominal fat and livers were removed and weighed immediately. The collected liver samples were immediately snap-frozen in liquid nitrogen and stored at −80 °C for expression analysis of lipid metabolism-related genes. Another portion of the liver was fixed in 4% paraformaldehyde for histological analysis. The relative weight of abdominal fat and liver was calculated as the weight of abdominal fat or liver in 100 g body weight (g/100 g BW). The severity of fatty liver was evaluated by liver color and scored, as modified based on a study conducted by Choi et al. (2012). The fatty liver was scored on a scale from 1 to 4 as follows: **FS1**, normal liver with dark red; **FS2**, mild case of FLHS with mild yellow liver and hemorrhages; **FS3**, moderate case of FLHS with light yellowish red liver and hemorrhages; and **FS4**, large and massive hemorrhages with putty-colored livers. The standard for the fatty liver score according to Avinash (2007) is indicated in Figure 1.

Experiment 2

To assess mRNA expression of lipid metabolism-related genes, a total of 30 laying hens were killed by electric shock at specified ages (15 at the age of 27 weeks and 15 at the age of 52 weeks). All livers were harvested and checked for fatty liver by gross examination. The livers with dark red color and no hemorrhages were determined as normal liver and livers with light yellowish red color and hemorrhages were considered as fatty liver. From each group (normal and fatty liver), 4-5 samples were pooled together for mRNA expression analysis of some lipid metabolism-related genes, including apolipoprotein B (*APOB*), peroxisome proliferator-activated receptor α (*PPARα*), *PPARγ, LPL*, and *FABP4*.

Experiment 3

To determine the changes in concentrations of some biochemical indicators, including TG, TC, ALT, AST, FABP4, and LPL, with age, blood samples from 40 laying hens were collected every 5 weeks from age 27 to 52 weeks. At age of 52 weeks, all 40 laying hens were killed by electric shock, and checked for fatty liver as described above.

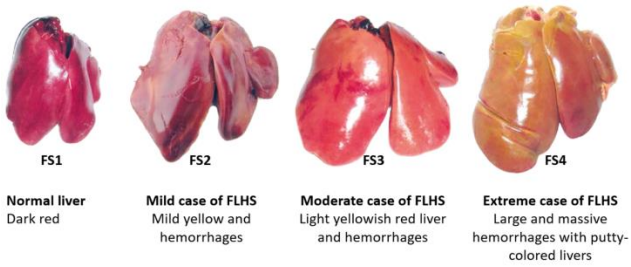

Figure 1. The standard for fatty liver score used for fatty liver examination in experiments 1-3. The color score, from 1 to 4 (from dark red to light yellowish-red), was judged by three investigators.

Histological analysis

The paraffin-embedded liver was cut into 5-μM sections and stained with hematoxylin and eosin. The degree of lipid accumulation was evaluated by the deposition of lipid droplets, which was quantified by ImageJ software (version 1.80, National Institutes of Health, Bethesda, MD, USA). The lipid accumulation was represented by the deposition of lipid droplets, with white pixel areas indicating fat vacuoles being divided by the total area scanned. The ImageJ software was used to quantify the staining of the liver section.

Biochemical analysis

Plasma samples were prepared by centrifugation (3,000 g for 15 min) and stored at –20 °C for future analysis. Concentrations of TG, TC, ALT, and AST were measured by colorimetric endpoint assays (A110-1-1, A111-1-1, C009-2-1, and C010-1-1 kits, respectively; Nanjing Jiancheng Bioengineering Institute, Nanjing, China). Total concentrations of plasma FABP4 and LPL were determined with chicken-specific commercial ELISA kits (Shanghai BlueGene Biotech Co. Ltd., China). Results were analyzed using the Thermo Multiskan Sky microplate reader (Thermo Fisher, Waltham, MA, USA). For liver TG and TC analysis, total proteins of liver were measured by bicinchoninic acid assay (kit A045-4-2; Nanjing Jiancheng Bioengineering Institute, Nanjing, China), the contents of liver TG and TC were measured by using kits A110-1-1 and A111-1-1, respectively (Nanjing Jiancheng Bioengineering Institute, Nanjing, China). All assays were performed according to the manufacturer's instruction.

Gene expression analysis

Chicken liver RNA was extracted using TRIzol Reagent (Invitrogen, Carlsbad, CA, USA) and checked on a Nanotrop Bioanalyzer (Agilent 2100; Palo Alto, CA, USA) for integrity analysis. The mRNA expression was detected by RT-qPCR in the liver. A PrimeScript RT reagent Kit (TaKaRa Biotechnology Co., Japan) was used to reverse transcribe RNA to cDNA, and qPCR was performed with SYBR Premix Ex Taq (TaKaRa Biotechnology Co., Japan) using an ABI Q5 Real-time PCR instrument (Applied Biosystems, Foster City, USA) at 95 °C for 30 s, followed by 35 cycles of 95 °C for 5 s, and 60 °C for 30 s. For RT-qPCR data analysis, each sample was run in triplicate. The mRNAs were normalized to *GAPDH* mRNA. The primer sequences are shown in Table 1. Data were analyzed using the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001).

Statistical analysis

Statistical analyses were carried out using SPSS version 21 (SPSS Inc., Chicago, IL, USA). Data were analyzed using one-way ANOVA and a *post hoc* Tukey test. P-value less than 0.05 was considered statistically significant. Spearman's correlation coefficient was used to test the relationship between various variables.

Table 1. Primers used in this study for RT-qPCR

Gene	Sequence (5'-3')
β-actin-F	AATGGCTCCGGTATGTGCAA
β-actin-R	GGCCCATACCAACCATCACA
GAPDH-F	GATGGGTGTCAACCATGAGAAA
GAPDH-R	CAATGCCAAAGTTGTCATGGA
PPARα-F	GCTTGTGAAGGTTGTAAGGGTT
PPARα-R	GACATTCCAACTGAAAGGCAC
PPARγ-F	GTCCTTCCCGCTGACCAAA
PPARγ-R	TCTCCTGCACTGCCTCCACA
FABP4-F	GGCCAAGCCTAATTTAACTATC
FABP4-R	TCCCATCCACCACTTTTCTC
APOB-F	ATACCCTGGGACTCTTGCCT
APOB-R	GAGAAGCTTTCAGGCTGGGT
LPL-F	ATTGCTGCCTCTTCTCCTTT
LPL-R	ATTGGTGACCTGCTTATGCTA

GAPDH: glyceraldehyde-3-phosphate dehydrogenase; PPARα: peroxisome proliferator-activated receptor α, PPARγ: peroxisome proliferator-activated receptor γ; FABP4: fatty acid-binding protein 4; APOB: apolipoprotein B; LPL: lipoprotein lipase.

RESULTS

Experiment 1

Liver and abdominal fat weight

In Experiment 1, different groups were significantly different in terms of BW ($P < 0.05$, Table 2). The amount of abdominal fat sequentially increased in chickens with

the increase of BW, although there was no significant difference between the normal BW and OW/Ob group ($P > 0.05$). The relative weight of abdominal fat was similar in both low and normal BW hens, whereas a significant increase of the relative weight of abdominal fat was observed in the overweight chickens (OW/Ob and SW/Ob groups), compared to the low BW group ($P < 0.05$). The relative weight of abdominal fat increased in the SW/Ob group, compared to the OW/Ob group ($P < 0.05$). There was no significant difference in the relative liver weight among chickens with different BW ($P > 0.05$). The concentration of TG was significantly higher in the SW/Ob hens, compared to the LW and the NW groups, while the obtained values of LW, NW, and OW/Ob hens were similar. The concentrations of TC were significantly lower in the LW laying hens than in the overweight hens (OW/Ob or SW/Ob), and the levels of AST were significantly increased in the NW, OW/Ob, and the SW/Ob groups in comparison to the LW hens. No significant differences in VLDL-C were observed among the four groups.

Correlation of body weight, relative weight of liver and abdominal fat with plasma markers

The abdominal fat pad weight, concentrations of TC and TG were significantly associated with BW ($P < 0.05$, Table 3). The concentrations of TC and TG were also positively correlated with the abdominal fat pad weight. The correlation between plasma TG and BW ($r = 0.662$) was stronger than that between plasma ALT and BW ($r = 0.108$), or plasma TC and BW ($r = 0.513$). Although other biomarkers were associated with each other (TG vs. ALT, $r = 0.224$; TG vs. TC, $r = 0.297$; VLDL-C vs. abdominal fad pad weight, $r = 0.169$), their correlations were insignificant. There was no significant correlation between liver weight and other biomarkers.

Table 2. Chicken body weights, relative weights of liver and abdominal fat, and plasma markers in the various body weight groups (Experiment 1)

Parameters	LW (n =15)	NW (n =15)	OW/Ob (n =15)	SW/Ob (n =15)
BW (g)	1665.71±40.03^{a}	1956.70±19.68^{b}	2084.43±14.17^{c}	2291.59±40.95^{d}
Relative weight, g/100 g BW				
Abdominal fat	2.49±0.21^{a}	3.05±0.27^{ab}	3.99±0.38^{b}	4.94±0.37^{c}
Liver	1.96±0.07	2.11±0.08	1.98±0.11	2.16±0.17
Plasma markers				
ALT(U/L)	17.03±2.68	11.36 ± 1.43	21.48±6.63	25.41±5.01
AST(U/L)	26.97±1.33^{a}	36.14±1.94^{b}	33.95±2.70^{b}	35.57±1.88^{b}
TC (mmol/L)	2.13±0.26^{a}	3.01±0.19^{ab}	4.13±0.50^{b}	3.57±0.27^{b}
VLDL-C (mmol/L)	2.25±0.21	3.64±0.50	2.95±0.34	3.34±0.76
TG (mmol/L)	13.45±1.10^{a}	16.58±1.20^{a}	23.17±2.09^{ab}	30.21±3.09^{b}

Values are expressed as mean ± SEM. ^{a,b,c} Mean values within a row with different superscript letters are significantly different ($P < 0.05$). ALT: Alanine aminotransferase, AST: Aspartate aminotransferase, TG: Triglyceride, TC: Total cholesterol, VLDL-C: Very low-density lipoprotein cholesterol, FS: Fatty liver score, BW: Body weight, LW: Low grade weight, NW: Normal weight, OW/Ob: Overweight/obese, SW/Ob: Seriously overweight/obese

Table 3. Spearman correlation coefficients among the chicken body weights, relative weights of liver and abdominal fat, and serum markers (Experiment 1).

Variables	TG	TC	VLDL-C	AST	ALT	Relative weight, g/100 g BW	
						Abdominal fat weight	Liver weight
BW	0.662**	0.513**	0.235	0.248	0.108	0.658**	0.085
TG		0.297	0.097	0.152	0.224	0.318*	0.057
TC			-0.024	0.299	0.018	0.349**	0.075
VLDL-C				0.142	-0.093	0.169	-0.107
AST					-0.257	0.257	-0.003
ALT						-0.033	0.057
Relative abdominal fat weight, g/100 g BW							-0.187

BW: Body weight, TG: Triglyceride, TC: Total cholesterol, VLDL-C: Very low-density lipoprotein cholesterol, AST: Aspartate aminotransferase, ALT: Alanine aminotransferase. * $P < 0.05$, ** $P < 0.01$.

Hepatic lipid accumulation

Pathological changes in the liver in all four groups at age 52 weeks are presented in Figure 2. The livers of overweight hens (OW/Ob and SW/Ob groups) were fragile and yellow, and some hemorrhagic spots appeared due to the high lipid accumulation when compared to layers with low BW (Figure 2a, b). The fatty liver score increased with BW. There was a significant increase in fatty liver score in the overweight groups (OW/Ob and SW/Ob groups), compared to the LW group ($P < 0.05$), while the fatty liver score in overweight hens (OW/Ob and SW/Ob groups) showed no significant difference between the two groups ($P > 0.05$, Figure 2c). However, the liver turned light yellow in the OW/Ob and SW/Ob groups indicating an increased fatty liver score, compared to the low and normal BW groups. To evaluate the consistency between liver lipid deposition and BW, the vacuolar areas of liver sections were quantified using image J software. The vacuolar area in the livers from overweight chickens (OW/Ob and SW/Ob groups) was significantly larger, compared to the low and normal BW groups ($P < 0.05$). No significant difference was observed between the two overweight groups (Figure 2d, $P > 0.05$). Concentrations of liver TG and TC were not significantly different in the chicken livers from the four groups ($P > 0.05$, Figure 2e).

Expression of lipid metabolism-related genes

The RT-qPCR analysis of lipid metabolism-related genes confirmed the changes in expression among the chickens with different levels of BW (Figure 3a). However, no regular expression of these genes was found among the layers with different BW values. As BW increased, *APOB* expression gradually decreased, and the mRNA expression of *APOB* decreased in the SW/Ob group compared to the LW group ($P < 0.05$), while it was not significantly different among the NW, OW/Ob, and SW/Ob groups ($P > 0.05$). Expression of *PPARα* was higher in the NW group, compared to the LW, OW/Ob, and SW/Ob groups ($P < 0.05$), however, no significant differences were observed among the three groups ($P > 0.05$). The mRNA expression of *FABP4* increased significantly in the NW, OW/Ob, and SW/Ob groups ($P < 0.05$), compared to the LW group, with the highest expression in the NW group. The expression of *PPARγ* was highest in the SW/Ob group, whereas there was no significant difference among the other three groups ($P > 0.05$). There was no significant difference in *LPL* mRNA expression among the four groups ($P > 0.05$) although it tended to increase with BW.

Plasma concentrations of FABP4 and LPL

Plasma concentrations of FABP4 and LPL in laying hens with different BW were also measured (Figure 3b). The concentration of FABP4 significantly increased as BW increased at age 52 weeks although no significant changes in LPL levels were observed among the four groups with different BW values. Plasma concentration of FABP4, measured by ELISA, was significantly upregulated and positively correlated with the fatty liver score (Figure 5c), indicating the diagnostic potential of plasma concentrations of FABP4. No significant correlation was found between plasma LPL and fatty liver score (data not shown).

Experiment 2

Increase of plasma FABP4 and LPL levels in chickens with fatty liver

To screen potential biomarkers in this chicken model of FLHS, five known lipid metabolism-related genes, including *APOB*, *PPARα*, *PPARγ*, *LPL*, and *FABP4* were selected for analyzing mRNA expression in normal and fatty livers. All samples from the laying hens of 52 weeks old were fatty liver. In laying hens of 27 weeks old, 12 out of 15 liver samples were normal; 3 liver with mild yellow color and hemorrhages were discarded from mRNA analysis. The results indicated that mRNA expression of *FABP4* and *LPL* significantly increased ($P < 0.05$), while the expression of *APOB*, *PPARα*, and *PPARγ* decreased ($P < 0.05$) in fatty livers, compared to normal livers (Figure 3c).

Experiment 3

Evaluation of changes in biochemical parameters with age of laying hens

The plasma concentrations of TG, TC, AST, ALT, FABP4, and LPL were measured in 40 laying hens every 5 weeks from age 27 to 52 weeks. The plasma concentrations of TG and TC displayed some variability among the individual layers. However, there was an increasing trend in TG levels with aging, compared to their concentrations in the laying hens at age 27 weeks (Figure 4a). At age 47 weeks, the concentrations of TG and TC were significantly higher than that at 32, 37, and 42 weeks. A significant decrease in the concentration of TC was observed in the plasma of the layers at age 52 weeks, compared to the obtained results at age 47 weeks, which was still higher than the obtained results of 27, 32, 37, and 42 weeks. No difference was found for the activities of ALT and AST among the six time points of

the layers although the activities of ALT and AST tended to increase with age. According to the recommended weight range, the experimental chickens were overweight since age 32 weeks (Figure 4b). From 27 to 52 weeks of age, plasma TG and TC concentrations were significantly correlated with BW ($r = 0.55$, $P < 0.01$ and $r = 0.61$, $P < 0.01$, respectively, Figure 4c). This trend in BW was consistent with the increasing trends of TG and TC concentrations. Plasma TG concentrations were positively associated with TC ($r = 0.68$, $P < 0.01$). The obtained results of ELISA revealed that FABP4 was significantly upregulated during 32-52 weeks of age (Figure 5a, $P < 0.05$). By age 52 weeks, the concentration of FABP4 and LPL was significantly higher than the age of 27 weeks ($P < 0.05$).

Correlation of FABP4 and LPL concentrations with other variables

Plasma FABP4 was positively correlated with LPL, TG, TC, and BW ($r = 0.29$, $r = 0.39$, $r = 0.20$, and $r = 0.31$, respectively, Figure 5b). Other markers were significantly associated with each other (LPL vs BW, $r = 0.18$; LPL vs TC, $r = 0.22$; and LPL vs TG, $r = 0.28$).

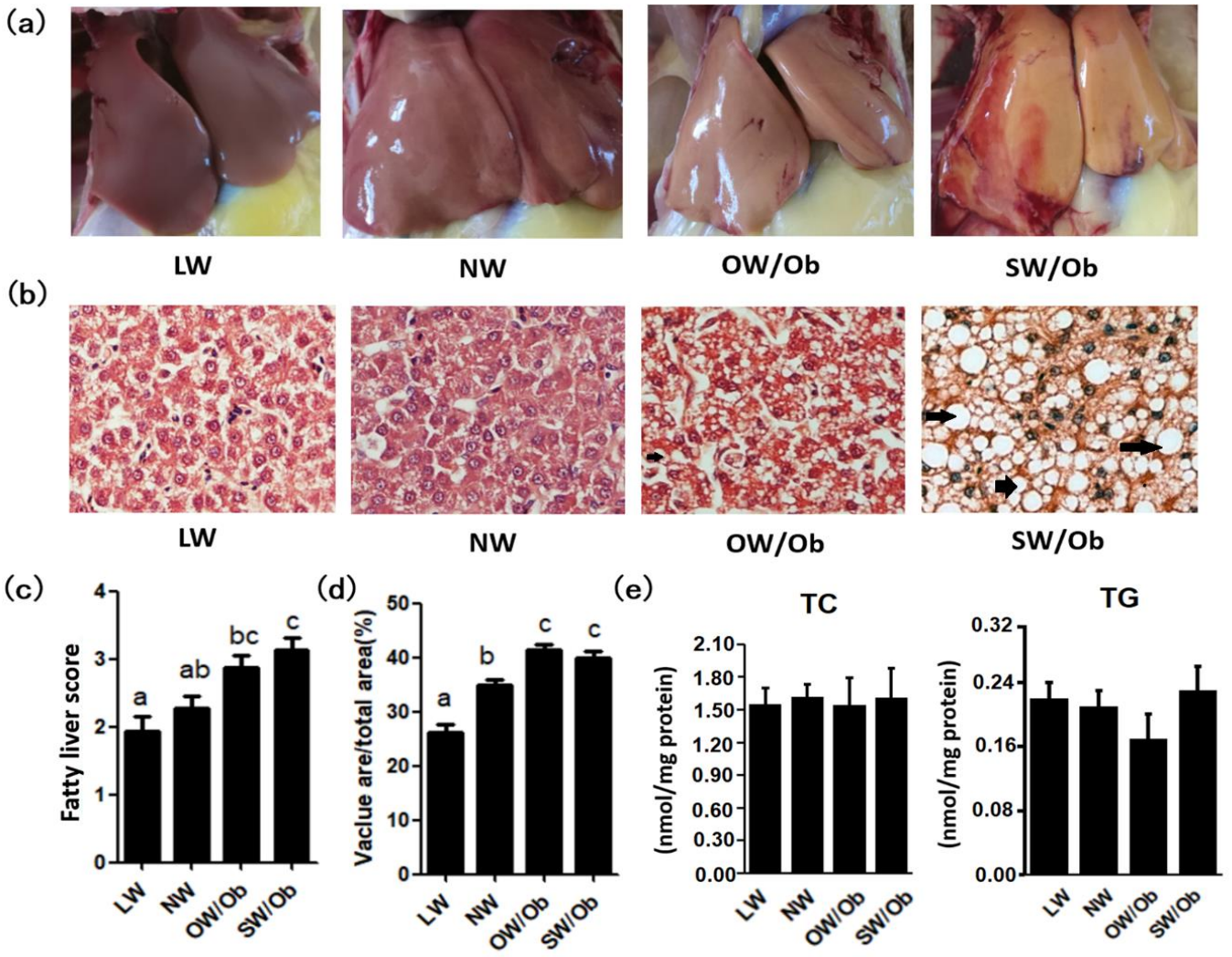

Figure 2. Results of evaluations of livers of chickens (52 weeks old) with different BWs. **a:** Representative images of various levels of liver hemorrhage. **b:** Representative images of histological sections of the liver after H&E staining. The arrow indicates the steatosis and lipid vacuolization inside the hepatocytes. Photographs were taken at 400× magnification. **c:** Mean fatty liver score in chickens with different BWs (score 1: normal liver with dark red; 2: mild case of FLHS with mild yellow liver and hemorrhages; 3: moderate case of FLHS, light yellowish red liver and hemorrhages; 4: severe case of FLHS, large and massive hemorrhages with putty-colored livers). **d:** Quantified results of fat vacuoles area within the liver section. **e:** Liver TG and TC concentrations in chickens with different BW. LW: Low body weight, NW: Normal body weight, OW/Ob: Overweight/obese, SW/Ob: Seriously overweight/obese, ALT: Alanine aminotransferase, AST: Aspartate aminotransferase, TG: Triglyceride, TC: Total cholesterol.

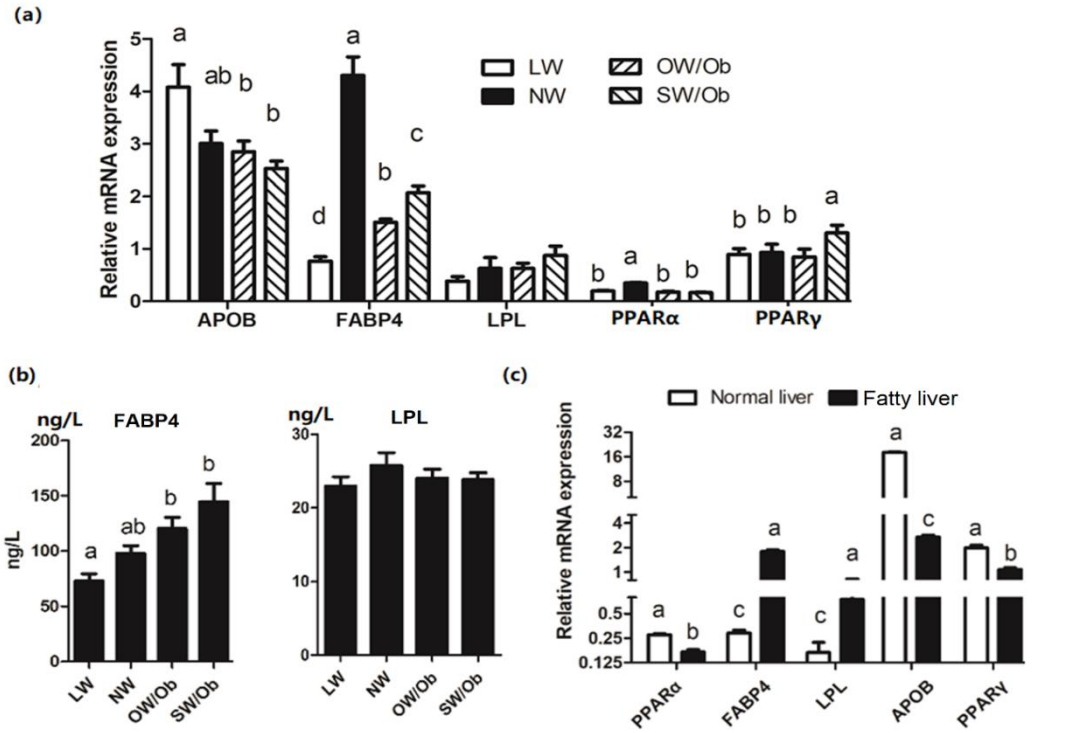

Figure 3. Evaluation of lipid metabolism-related parameters in relation to BW and liver condition. **a:** RT-qPCR analysis of lipid metabolism-related genes in livers of laying hens with different BW. **b:** Chicken plasma concentrations of FABP4 and LPL in laying hens with different BW (n = 15/BW group). **c:** RT-qPCR analysis of lipid metabolism-related genes in normal and fatty livers collected from laying hens of 27 and 52 weeks old, respectively. FABP4: Fatty acid-binding protein 4, LPL: Lipoprotein lipase, BW: Body weight, LW: Low body weight, NW: Normal body weight, OW/Ob: Overweight/obese, SW/Ob: Seriously overweight/obese.

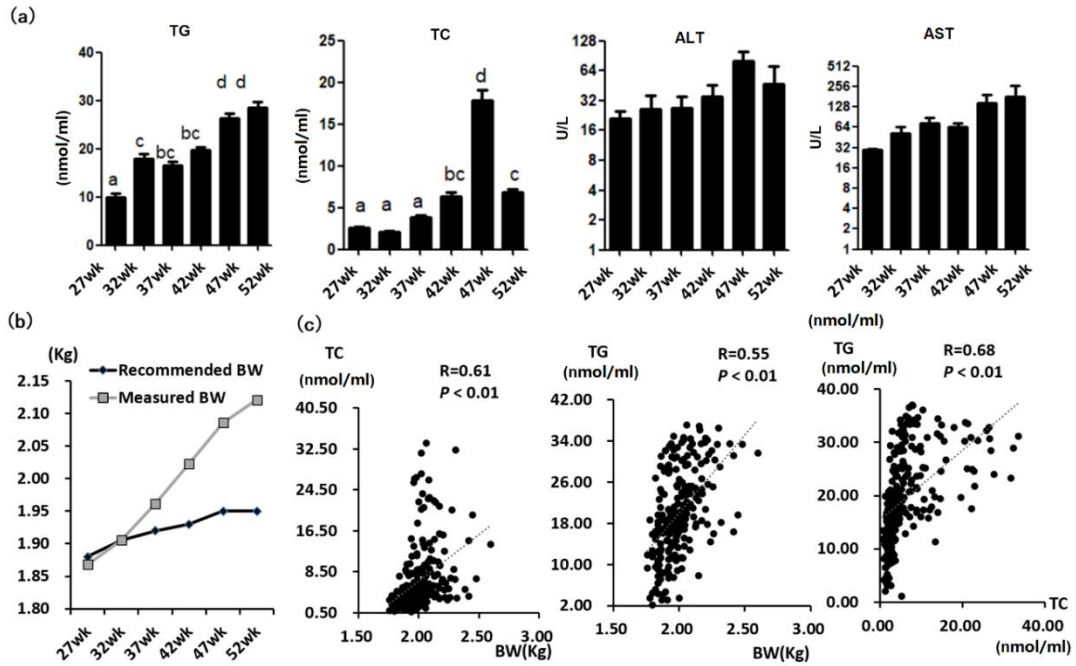

Figure 4. Evaluation of changes in biochemical parameters with age of laying hens. **a:** Plasma concentrations of TG, TC, ALT, and AST at six time points in laying hens. **b:** Comparison of measured BW of laying hens at different ages with recommended BW. **c:** Correlation of BW with TG and TC; Correlation of TG with TC. Values are expressed as mean ± SEM. ALT: Alanine aminotransferase, AST: Aspartate aminotransferase, TG: Triglyceride, TC: Total cholesterol, FLHS: Fatty liver hemorrhagic syndrome, BW: Body weight.

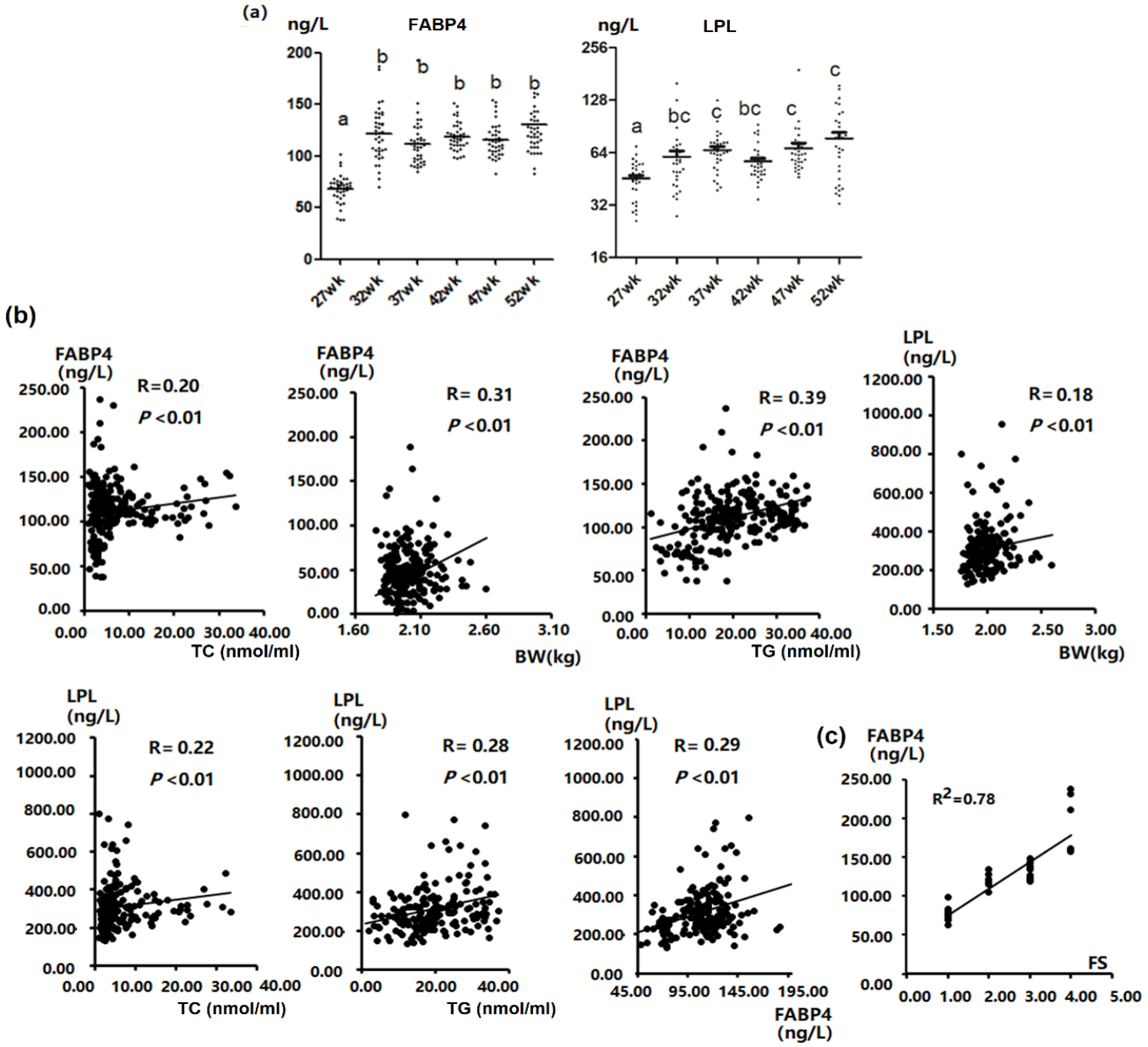

Figure 5. Evaluation of changes in FABP4 and LPL levels with age of laying hens. **a:** Scatter dot plot showing plasma concentrations of FABP4 and LPL in laying hens (n = 40) at different ages. **b:** Spearman's correlation analyses between FABP4 and LPL concentrations and other variables using data measured from 27 to 52 weeks of age. **c:** Correlation between plasma concentrations of FABP4 and FS of chickens (FS1: normal liver, n = 13; FS2: mild FLHS, n = 12; FS3: moderate FLHS, n =15; FS4: severe FLHS, n =10). FS: Fatty liver score, FABP4: Fatty acid-binding protein 4, LPL: Lipoprotein lipase, BW: Body weight.

DISCUSSION

FLHS is a metabolic disease characterized by excessive fat accumulation in the liver, accompanied by a hemorrhagic and pale liver, causing sudden death of laying hens (Shini et al., 2012). Signs of this metabolic disease are difficult to identify when the birds are alive, and it can only be determined through dissection. Therefore, it is urgent to find reliable noninvasive biomarkers to diagnose FLHS and monitor laying hens at an earlier time point when diet changes and potential health treatments can be used purposefully. The present study examined the relationship between BW and serum lipoproteins, and identified FABP4 as a potential novel circulating biomarker of FLHS.

Based on findings addressing production, aged layers have an increased risk of FLHS, and the BW of these layers is always higher than recommended values in the breeding manual (Dong and Tong, 2019). Previous studies have indicated that the occurrence of FLHS is the result of abnormal accumulation of liver fat, mainly due to the large increase in liver TG, and the abnormal accumulation of fat caused by dysfunction in liver fat metabolism (Dong and Tong, 2019; Shini et al., 2019; Zhuang et al., 2019; Shini et al., 2020). The present study demonstrated that concentrations of TG, TC, and VLDL-C were positively correlated with BW in aged laying hens, and the amount of abdominal fat and the concentration of TG in aged layers significantly increased with BW gain. Lipid accumulation and hemorrhage were more severe in the overweight layers of the low BW group. These results suggested that the higher the weight, the higher the risk of FLHS in aged layers. However, it is worth noting that no difference was observed in the relative liver weight and the concentration of VLDL-C among chickens with different values of BW. The concentrations of TG were also similar among the NW and OW/Ob group hens. Also, the relative weight of abdominal fat was similar between LW and NW hens. In addition, no significant difference in the fatty liver score was observed between layers in adjacent BW groups. Based on this, it can be found that the differences between layers in adjacent BW groups were relatively small, and BW within the standard range recommended by the manufacturer could not be used as an indicator of FLHS in aged layers. Thus, these findings indicated that BW of laying hens should be monitored at all times during production, but BW cannot be used as the sole criterion to discriminate aged laying hens with liver steatosis.

TG represent the main form of storage and transport of fatty acids in cells and circulating system, and they have been suggested to have the potential for diagnosis of NAFLD (Safaei et al., 2016). Evidence also suggests that TC is a risk factor for NAFLD, and as the level of TC improves, the incidence of NAFLD increases as well (Ballestri et al., 2016; Ren et al., 2019). High levels of TG and TC were also reported in previous studies in laying hens with FLHS (Dong and Tong, 2019; Gao et al., 2019). To find potential serum markers for early prediction of FLHS, changes in the plasma concentrations of TG and TC were examined every 5 weeks from 27 weeks (normal liver) to 52 weeks (FLHS was confirmed through dissection at the end of the experiment) of age in 40 laying hens. Furthermore, the serum activities of AST and ALT were examined during this period as liver injury indicators. It was found that TG and TC levels, which were positively associated with BW, increased as chickens grew older. This means that TG and TC are good risk markers for FLHS although further confirmation is needed since the current study did not address the correlation of FLHS morphology with TG and TC levels at different periods. Furthermore, no difference was found in the activities of ALT and AST among the six time points, indicating that the classic liver injury indicators, AST and ALT, were unable to predict chicken FLHS, which was consistent with the conclusion drawn for NAFLD (Ekstedt et al., 2006). The results were also in line with a previous study conducted by Diaz et al. (1999) who found no clear correlation between plasma enzyme activities (AST, ALT, and lactate dehydrogenase) and the degree of liver hemorrhage in laying hens.

Finally, five known lipid metabolism-related genes, *APOB*, *PPARα*, *PPARγ*, *LPL*, and *FABP4*, were selected for mRNA expression analysis in fatty and normal livers. Expression of *APOB*, *PPARα*, and *PPARγ* decreased in fatty livers, compared to the normal liver as opposed to the results reported by Li et al. (2015). They analyzed the liver transcriptome of young chickens (age 20 weeks) and laying hens (age 30 weeks) by sequencing, and found that the mRNA levels of fatty acid uptake and transport (*PPARγ*, *APOB*, and *FABP3*) increased in the liver of laying hens (Li et al., 2015). This difference may be due to the age of the birds studied. The current study examined the expression of lipid metabolism-related genes in the liver of aged chickens with FLHS, while Li et al. (2015) focused on younger birds at peak production. A similar result was reported by Song et al. (2017), in which obvious decreases in apolipoprotein (apo) A-I and apoB100 levels were observed in the hepatic tissues. The authors reported that expression of apoA-I decreased on day 60 while the apoB100 levels slightly increased on day 30 and then decreased on day 60 in the liver of an FLHS model induced by a low-protein high-energy diet, and they speculated that this decrease was due to liver injury from FLHS (Song et al., 2017). APOB plays an important role in the hepatic export of triacylglycerols by interacting with TG, cholesterol, and phospholipids (Kessler et al., 2014; Devaraj and Jialal, 2020). The fatty acid oxidation related gene *PPARα*, together with *PPARγ* and *PPARβ/δ*, is involved in many aspects of lipid metabolism (Bougarne et al., 2018). Hepatocyte PPARα deletion impairs fatty acid catabolism resulting in hepatic lipid accumulation (Gao et al., 2015; Montagner et al., 2016). Hence, the downregulation of *APOB* and *PPARα* may contribute to the hepatic lipid accumulation in the liver of aged laying hens with FLHS as suggested by Lu et al. (2019).

The mRNA expression of *FABP4* and *LPL* significantly increased in the liver of FLHS chickens. FABP4 is an important lipid chaperone that plays an important role in lipid-mediated cellular physiological processes and metabolism. FABP4 is mainly expressed in adipocytes and macrophages, and high expression of FABP4 is closely related to the metabolic syndrome caused by obesity (Kralisch and Fasshauer, 2013). Elevated expression of hepatic FABP4 is positively correlated with the severity of NAFLD (Thompson et al., 2018). High levels of serum FABP4 are also reported in NAFLD patients, however, its use as a prognostic marker in serum is still controversial (Koh et al., 2009; Kim et al., 2011; Coilly et al., 2019). LPL transports plasma lipids into tissues and plays an important role in the regulation of lipid metabolism and energy balance (Li et al., 2014). In contrast, there is almost no LPL expression in normal adult liver, while increased hepatic *LPL* mRNA expression is observed in obese humans, which is postulated to contribute to hepatic TG accumulation (Pardina et al., 2009). Consistent with the obtained results of NAFLD, mRNA analysis indicated that expression of *FABP4* and *LPL* was upregulated in the liver of laying hens with FLHS. Plasma FABP4 and LPL concentrations sequentially increased in chickens with increased BW indicating that plasma FABP4 and LPL might be risk markers for FLHS in laying hens. Accordingly, there was a positive correlation between the plasma level of the FABP4 and the severity of fatty liver in aged laying hens suggesting that FABP4 might be a potential diagnostic marker for FLHS.

CONCLUSION

In conclusion, plasma TC, TG, FABP4, and LPL are positively associated with BW, and risk of FLHS. Determination of these biomarkers in plasma samples from FLHS hens could provide a rapid and first-line diagnosis of FLHS for clinical application.

DECLARATIONS

Acknowledgments

This work was supported by the SAAS Program for Excellent Research Team (SPERT) under Grant (B-03) and China Agriculture Research System under Grant (CARS-40-K03).

Competing interests

The authors declare that they have no competing interests.

Author contributions

Professor CY supported the funding. Dr RL and CX did the RT-qPCR and ELISA assay. Mr NW, Mr GZ, and Ms YT collected the samples. Associate professor LZ designed the experiments, analyzed the data, did the experiments, and wrote the manuscript. All authors read and approved the final manuscript.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 556-564, December 25, 2020

Research Paper, PII: S2322455X2000063-10

DOI: https://dx.doi.org/10.36380/jwpr.2020.63

Immune-Complex Infectious Bursal Disease Virus versus Live Attenuated Vaccines to Protect SPF Chicken against Very Virulent Virus Challenge

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Received: 24 Sept. 2020
Accepted: 05 Nov. 2020

ABSTRACT

In this study infectious bursal disease (IBD) vaccinations were evaluated against very virulent IBD (vvIBDV) challenge and were compared. A total of 120-day-old white Leghorn SPF chickens were divided into 6 groups (each was 20 birds). Two groups were vaccinated on either day 1 with an immune-complex vaccine. The second groups were vaccinated at days 9 and 14 of age using intermediate and intermediate plus IBD vaccines, respectively the balance groups are controls. All vaccines were administered according to the manufacturer's instructions. The challenge was conducted on the 16 days of age using 10^5 EID_{50} /0.1 ml of a vvIBDV strain via the oculonasal route. The antibody immune response was monitored in all groups at 14, 21, 28, and 35 days of age. The performance, bursal gross lesions, challenge virus detection, and bursal histopathology were evaluated in vaccinated non challenged and vaccinated challenged birds at days 21 and 28 of age. All vaccinated groups were protected against the vvIBDV challenge compared to 40% mortality in the challenge control group. Both the immune-complex and live attenuated IBD vaccine groups showed similar bursa body weight (BB) ratios compared to the negative control group. The immune-complex vaccinated groups antibody titers were significantly higher except on 28th day of age. Upon challenge, the intermediate/intermediate plus vaccinated challenged group showed higher antibody titers at 21 and 35th with the challenge virus detection and quantification on day 28. The immune-complex vaccinated challenged group developed milder bursal histopathology signs but no differences between the 2 vaccine programs were seen. It can be understandable, the use of either immune-complex vaccine at day-old or early vaccination with intermediate followed by intermediate plus live attenuated IBD vaccines induced protective antibody titers and protect chickens against an early vvIBDV challenge. The suggested schedules need further evaluation in commercial broilers with maternal derived IBD antibodies to simulate field conditions.

Keywords: Immune-Complex vccine, Infectious Bursal Disease, Live Attenuated Vaccine, SPF Chicken

INTRODUCTION

Infectious Bursal Disease (IBD) is an acute and highly contagious disease in chickens at 3 weeks of age and older causing high mortality and immunosuppression leading to a variety of secondary infections and a decreased response to vaccinations (Eterradossi and Saif, 2020). IBDV belongs to the *Birnaviridae* family within the genus Avibirnavirus (Delmas et al., 2019). The virus is non-enveloped, single shelled with a diameter of 60 to 70 nm (Alkie and Rautenschlein, 2016).

IBDV has a predilection for the immature actively dividing B lymphocytes and causes lytic infection of IgM bearing B cells resulting in the decrease in circulating IgM^+ cells (Sivanandan and Maheswaran, 1980; Dey et al., 2019). Infected chicken produces less level of antibodies against the antigen (Ingraoet al., 2013). IBDV induced humoral deficiency is reversible and overlaps with the restoring of bursal morphology (Sharmaet al., 2000).

Three main clinical symptoms of the disease were reported and include the classical form caused by the classic moderate virulent strains of IBDV and manifested by acute depression followed by typical signs and lesions with 10–50% mortality. The acute form is caused by very virulent strains of IBDV (vvIBDV) characterized by acute progressive and typical clinical signs resulting in high mortality rates on affected farms (50–100%) (Stoute et al., 2009; Ewies et al., 2017; Eterradossi and Saif, 2020). Finally, the immunosuppressive form, principally described in the United States, is caused by low-

pathogenicity strains of IBDV and variant strains (e.g. Delaware strains) with few clinical signs, no mortality but with marked bursal lesions and concurrent infections with other agents (Dey et al., 2019; Shehata et al., 2019).

The available live vaccines against IBDV are categorized as "mild", "intermediate" and "hot" according to their degree of virulence (Rautenschleinet al., 2003). Killed virus vaccines in oil-adjuvant can prolong the duration of immunity in breeder flocks in addition to containing both standard and variant IBDV strains. Therefore, maternal antibody profiling of the breeder flock should be done to assess the effectiveness of vaccination and the persistence of antibody (Eterradossi and Saif, 2020). Mild vaccines are not very effective in the presence of high levels of maternal antibodies or against very virulent strains of IBDV. Intermediate and hot vaccines are much more effective but may induce moderate to severe lesions in the bursa of Fabricius (BF) (Camilotti et al., 2016).

To overcome the problem of maternal immunity interference, the IBDV vectored vaccines were developed. For instance, herpesviruses expressing the surface viral protein 2 (VP2) of IBDV (Perozo et al., 2009) and immune complex vaccines containing an IBDV-specific antibody and live-attenuated IBDV (Schat et al., 2011). Both types are commercially available and administered in-ovo or at one-day of age without maternal immunity interference (Muller et al., 2012).

In this study, the administration of immune-complex IBD vaccine (Bursaplex®) at day-old was compared with the use of an intermediate followed by an intermediate plus vaccines at 9 and 14 day-old, respectively, in SPF chickens. The comparison items included the clinical protection, bursal pathology, serology as well as detection and quantification of the challenge virus.

MATERIALS AND METHODS

Ethical approval

All experimental procedures were reviewed and approved by the Faculty of Veterinary Medicine, Zagazig University, Egypt (FVM/ZAG-191207).

Vaccines and viruses

Bursaplex® (Zoetis, USA) is an immune-complex IBD vaccine that contains an embryo origin IBD live strain in conjunction with bursal disease antiserum and recommended for subcutaneous injection of chickens at one day of age. Bursine®-2 "intermediate live attenuated IBD vaccine" and Bursine plus® "intermediate Plus live attenuated IBD vaccine" (Zoetis, Belgium) were used. The challenge vvIBDV strain BSU-03-2016 (acc.no. KX077978) was retrieved from the repository of the Poultry Diseases Department, Faculty of Veterinary Medicine, Beni-Suef University, Egypt. The virus was propagated and titrated in 11 day-old SPF embryonated chicken eggs (Eterradossi and Saif, 2016).

Experimental design

A total of 120-day-old white Leghorn SPF chickens were divided into 6 groups (20 birds) placed in a negative pressure chicken isolator. Birds were vaccinated on either day 1 or days 9and 14 of age according to the experimental design summarized in table 1. All vaccines were administered according to the manufacturer's instructions. The challenge was conducted on the 16th day of age using 10^5 EID_{50} /0.1 ml of the vvIBDV strain via the oculonasal route (Eterradossi and Saif, 2016).

IBDV ELISA testing

Collected chicken sera were checked for IBD specific antibodies using ID Screen® IBD Indirect ELISA kit (IDvet, France) according to manufacturer instructions.

IBDV RT-PCR detection

Vaccinal and vvIBDV detection and quantification in 5 pooled bursal homogenates collected at the 28th day of age were conducted using qualitative Kylt® IBDV Pathotyping kits (AniCon Labor GmbH, Germany). The RNA was extracted using Kylt® RNA/DNA Purification kit (AniCon Labor GmbH, Germany) according to the manufacturer's instructions. The reaction performed in a 20 µl volume consisted of 10 µl of 2x RT-qPCR-Mix, 6 µl of Detection-Mix, and 4.0 µl of the tested RNA samples. The Kylt® kit thermal Profile III was; reverse transcription at 50 °C for 10 min, activation of Polymerase at 95 °C for 1 min, and 42 cycles of Denaturation at 95 °C for 10 sec, annealing and extension at 55°C for 1 min. The fluorescence detection channels were fluorescein (FAM) for vvIBDV, Cy5 for vaccinal IBDV, and Hexachloro-Fluorescein (HEX) for the internal kit control.

Histopathology

The bursa of Fabricius, thymus, spleen, and kidneys were collected from 5 chickens at 21 and 28th days of age. The formalin-fixed paraffin-embedded specimens were sectioned (4–5 µm) and stained with hematoxylin and

eosin stain and examined microscopically (Suvarna et al., 2018).

Statistical analysis

The differences in body weights, bursal body weight ratios (bursal weight/bodyweight×1000), and ELISA antibody titers were estimated using one-way ANOVA with multiple comparison Tukey's post-test through GraphPad Prism version 5.00 for Windows (GraphPad Software, San Diego California USA, *www.graphpad.com*).

Table 1. Experimental design of different vaccination schedules, sampling, and sample testing

Groups	Vaccination	Challenge at 16th day[1]	Monitoring, sampling, and measurements
Control negative	-	-	- ELISA: IBD ELISA at 0 day - Daily monitoring for clinical signs and mortality - At 14,28,35th day • Serology (IBD ELISA) - On 21,28Th day: • Body weights, and Bursa/body weight ratio • Histopathology • IBD PCR
Bursaplex	1st day: Bursaplex	-	
Interm./Interm. plus	9th: intermediate IBD vaccine 14thday: intermediate plus IBD vaccine	-	
Bursaplex- CH	1st day: Bursaplex	+	
Interm./Interm. Plus-CH	9th: intermediate IBD vaccine 14thday: intermediate plus IBD vaccine	+	
Challenge control	-	+	

[1] Challenge was conducted on the 16th day of age using 10^5 EID_{50} /0.1 ml of the vvIBDV strain via the oculonasal route

RESULTS

Clinical protection of immune-complex and live attenuated IBD vaccines

All vaccinated groups were protected against the vvIBDV challenge. Meanwhile, birds in the challenge control group showed 40% mortalities between day 4 and 5 post-challenge (Table 2). Upon necropsy, the challenge control group showed typical IBD lesions including hemorrhage on the thigh and breast muscle as well as bursal inflammation and enlargement. In vaccinated groups, mild bursal enlargement was noticed. no significant differences in body weights though lower body weights were observed in all groups compared to the negative control group (Table 2).

Bursa body weight ratio

Bursal body weight ratios (BB ratios) were more indicative of the clinical protection afforded by different vaccines. Both Bursaplex and intermediate/intermediate plus vaccinated non challenged groups showed higher BB ratios compared to the negative control group. The BB ratios were always significantly lower than the challenge control group especially in the Bursaplex vaccinated challenged group at 28 days of age (Figure 1).

IBDV serology in vaccinated and vaccinated challenged groups

As shown in figure 2, the ELISA antibody titers in the vaccinated nonchallenged groups were relatively higher in Bursaplex vaccinated groups at 14 and 21 day-old compared to the intermediate/intermediate plus vaccinated group. However, both groups showed no differences at 28 days of age, but the antibody titers decay was faster in the intermediate/intermediate plus vaccinated group at day 35 (figure 2A). No significant differences between the vaccination regimes upon challenge, however, the intermediate/intermediate plus vaccinated groups showed relatively higher titers (figure 2B).

Challenge virus detection and quantification

The challenge virus detection and quantification on the 28th day of age are shown in table 3. The vvIBDV was evident in the intermediate/intermediate plus vaccinated group however, no challenge virus detection was observed in the Bursaplex vaccinated challenged group. The virus was confirmed to be vvIBDV by partial sequencing of the VP2 gene (data not shown)

Histopathology

At 21 days of age, no significant bursal changes were observed in Bursaplex or Intermediate/intermediate plus vaccinated non-challenged groups except for slight B-cell proliferation of the cortical medullary cells with normal mucosal folds of the bursa in the Intermediate/intermediate plus vaccinated non-challenged group (figure 3C). Similarly, upon challenge no prominent changes while the

Bursaplex vaccinated challenged group showed lymphoproliferative follicular tissue with highly activated cortical lymphocytes (figure 3D). The challenge control showed massive degenerative changes, central necrosis and apoptosis, inflammatory cell infiltration, and aggregations of necrotic and apoptotic (Figure 3F).

By the 28th day of age, similar bursal appearance in the vaccinated non challenged groups were observed (Figure 4 B and C). In the vaccinated challenged groups, the Bursaplex vaccinated group showed a well-formed healthy epithelial lining of the pica and characteristic lymphoproliferative follicular tissue, and the cortical lymphocytes were highly activated and appeared with compacted deep basophilic nuclei and scanty cytoplasm (Figure 4D). The Bursa of intermediate/intermediate plus vaccinated challenged chickens' group is showed multiple immune-reactive lymphoid follicles and mild thickening of the interstitial connective tissue by fibroblastic proliferation (Figure 4E). The challenge control group bursae showed medullary massive central necrosis, apoptosis, and sometimes heterophilic infiltration. The cortical layer appeared completely necrotic with the disappearance of almost all the lymphoid cells (Figure 4F).

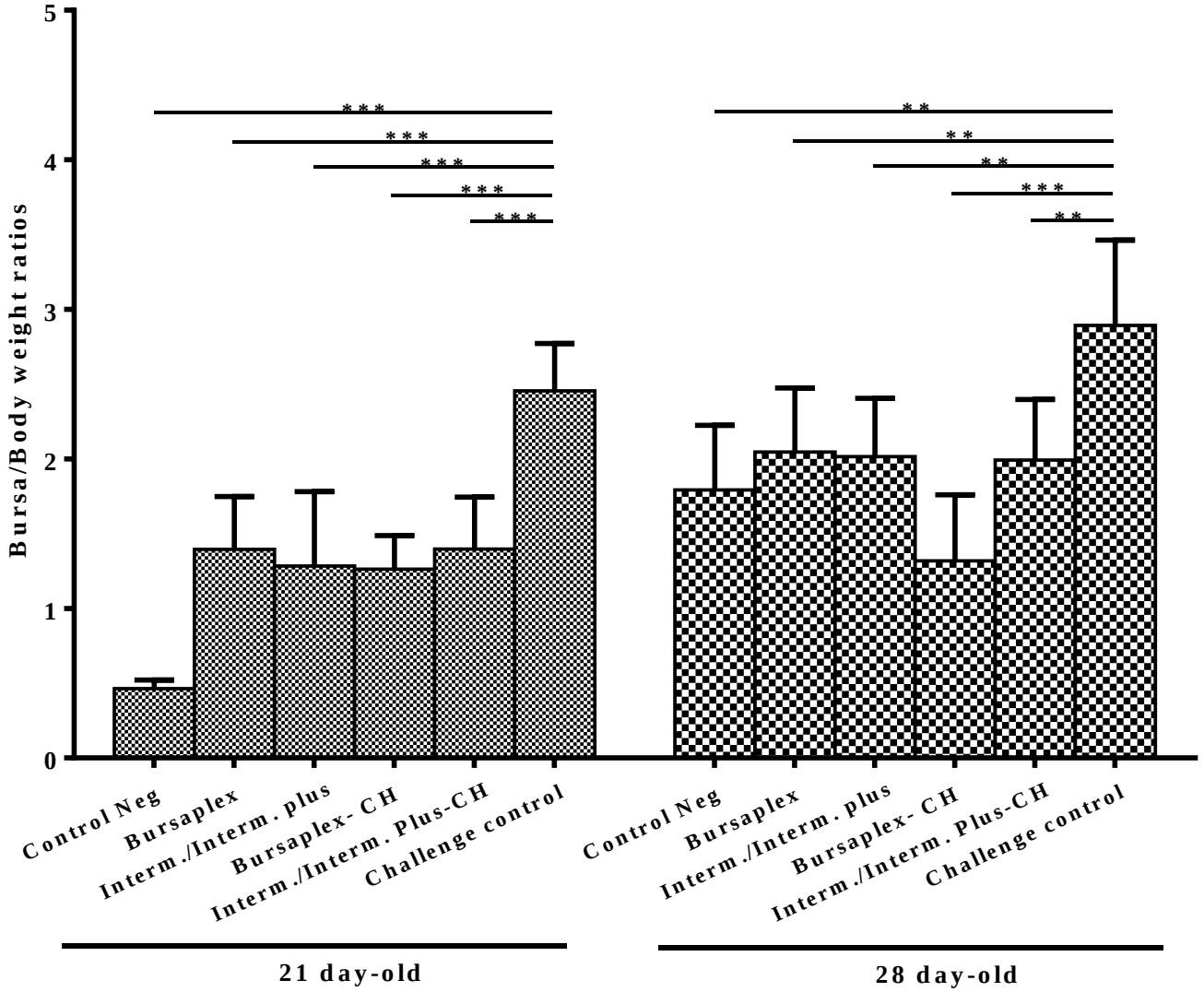

Figure 1. Bursa body weight ratios in different experimental groups at 21 and 28 day-old**.** The stars indicate significant differences at *≤0.05, **≤0.001, ***≤0.0001

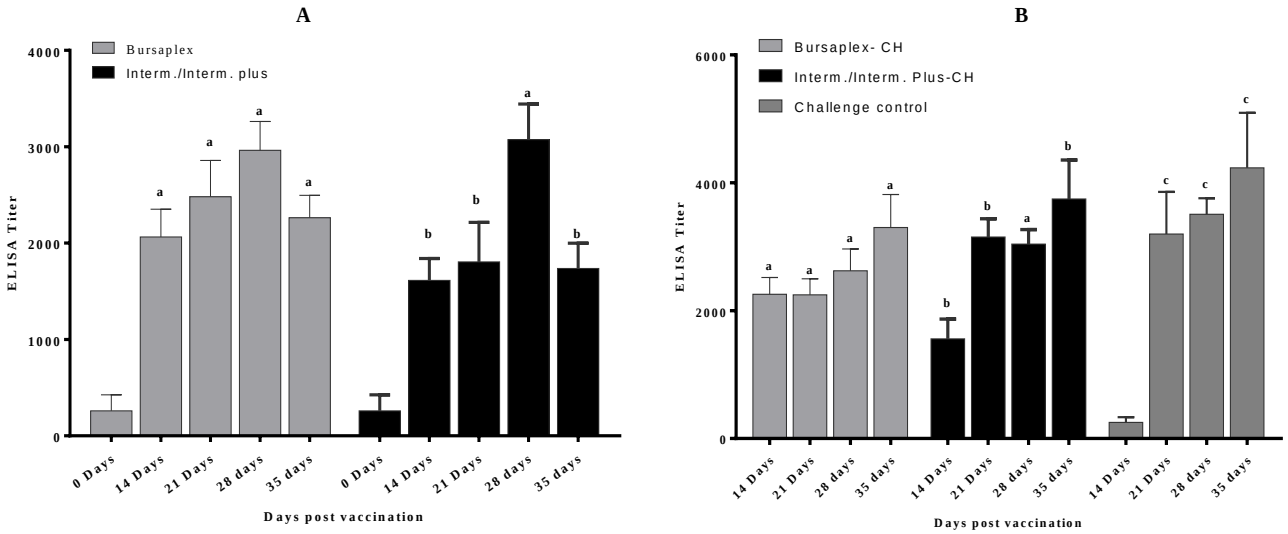

Figure 2. ELISA antibody titers in vaccinated non challenged (A) and vaccinated challenged groups (B) at 14, 21, 28, and 35 day-old. Bars with different small letters at the same time point are significantly different ($p \leq 0.05$)

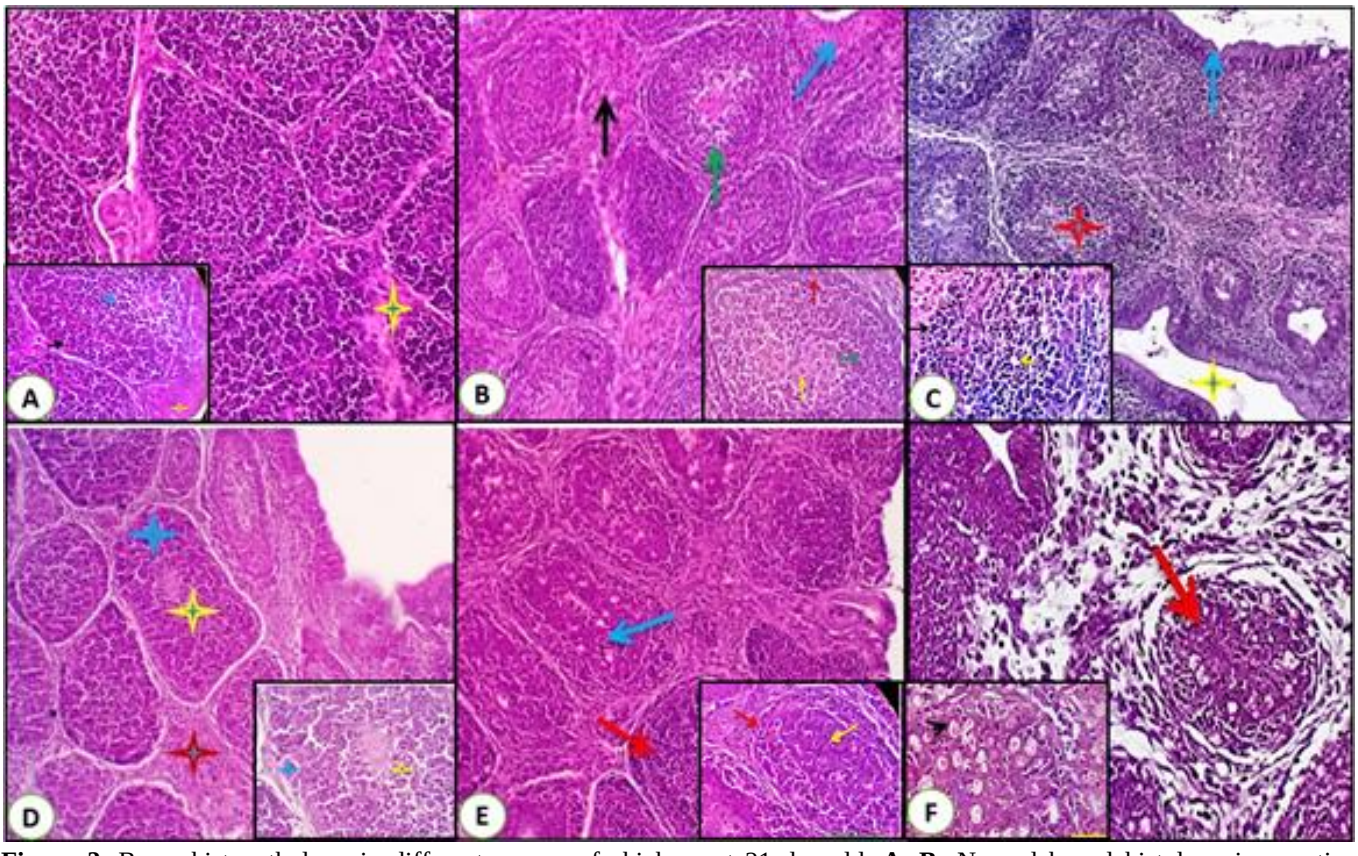

Figure 3. Bursa histopathology in different groups of chickens at 21 day-old. **A, B:** Normal bursal histology in negative control and Bursaplex vaccinated non-challenged group. **C**: Intermediate/intermediate plus vaccinated non challenged group showing slight B-cell proliferation of the cortical medullary cells (red and yellow arrow) with normal mucosal folds of the bursa (blue arrow). **D:** Bursaplex vaccinated challenged group showing lymphoproliferative follicular tissue with prominent central medullary lymphocytes (yellow stars) and the cortical lymphocytes were highly activated (dark blue stars). **E:** Intermediate/intermediate plus vaccinated challenged group showing normal bursal folds and immune-reactive lymphoid follicles. **F:** Challenge control showing degenerative changes (red arrows), massive central necrosis and apoptosis, inflammatory cells infiltration with the presence of aggregates of necrotic and apoptotic debris (black arrowhead).

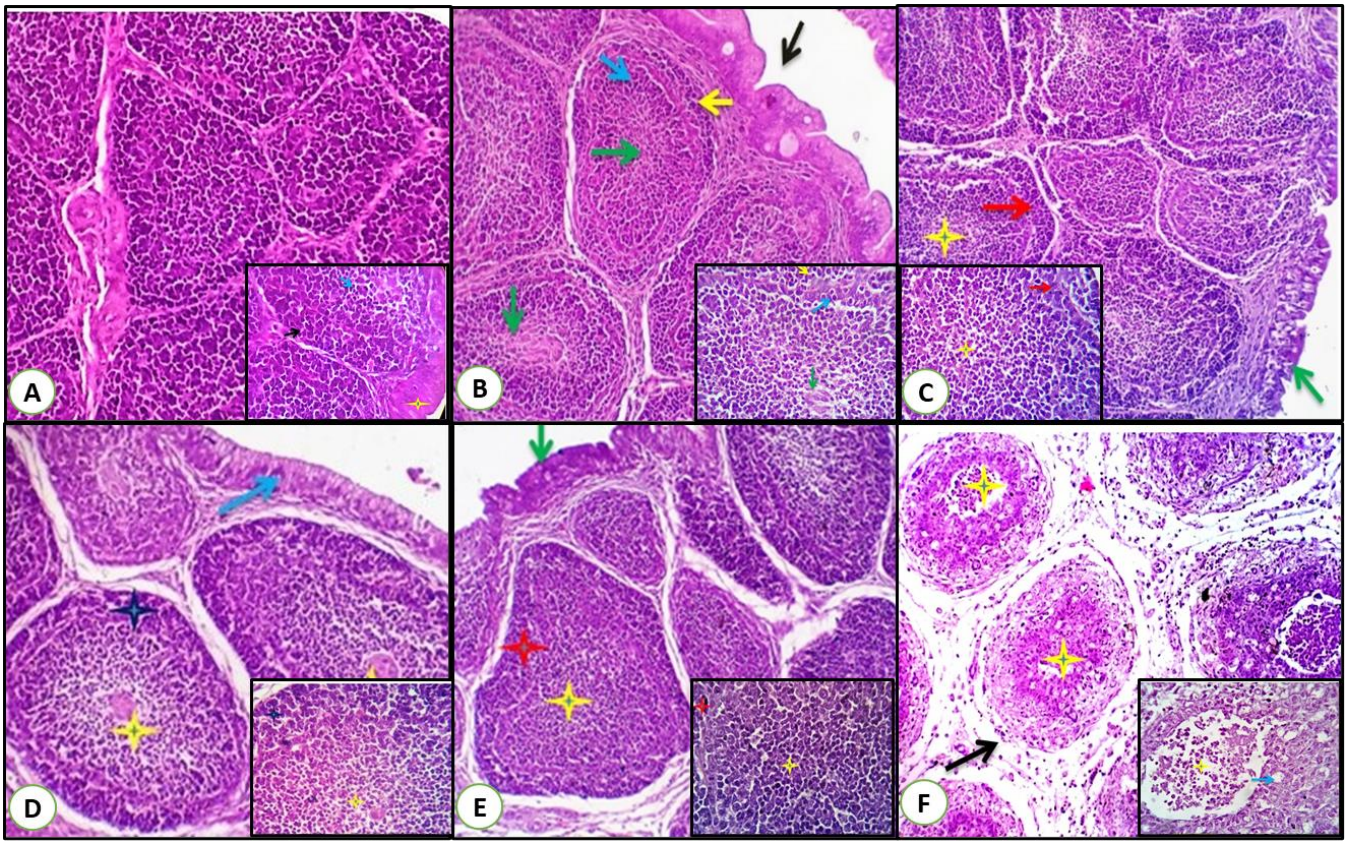

Figure 4. Bursa histopathology in different groups at 28 day-old. A: normal bursal histology in the negative control group. **B:** Bursaplex vaccinated non challenged group showing mucosal folds clear margins of the follicles, a layer of undifferentiated epithelial cells occupied the periphery of the medulla (green arrows). Both cortical (blue and yellow arrows) and medullary cellular contents (green arrows) are moderately reactive with closely backed small and large lymphocytes. **C:** intermediate/intermediate plus vaccinated non challenged group showing large sized follicles with proliferation of the cortical (red arrows) and medullary cells (yellow stars), the medullary centers appear slightly pale and crowded by large proliferating B-cells (yellow stars). **D:** Bursaplex vaccinated challenged group showed healthy epithelial lining of the pica (blue arrow) and lymphoproliferative follicular tissue (yellow stars), highly activated cortical lymphocytes with deep basophilic nuclei, and scanty cytoplasm (dark blue stars). **E:** intermediate/intermediate plus vaccinated challenged group showing normal bursal folds (green arrows), multiple immune-reactive lymphoid follicles (red stars and yellow stars), and mild thickening of the interstitial connective tissue by fibroblastic proliferation (green star). **F:** challenge control group showing massive medullary necrosis, apoptosis, heterophilic infiltration with central aggregates of necrotic and apoptotic debris (yellow stars and black arrows), the cortical layer appeared completely necrotic with the complete lymphoid cell depletion (blue stars).

Table 2. Daily mortalities and protection percent in different vaccinated chickens against vvIBDV challenge

Challenge	Groups	Daily Mortalities (days post-challenge)						Protection %
		3	4	5	Live	Dead	Total	
No	Negative control	-	-	-	20	0	20	100
	Bursaplex[1]	0	0	0	20	0	20	100
	Interm. /Interm. Plus[2]	0	0	0	20	0	20	100
Yes	Bursaplex- CH[1]	0	0	0	20	0	20	100
	Interm. /Interm. Plus-CH[2]	0	0	0	20	0	20	100
	Challenge control	0	5	3	12	8	20	40

[1]Vaccination schedule: 1st day: Bursaplex [2]Vaccination schedule: 9th: intermediate IBD vaccine- 14thday: intermediate plus IBD vaccine

Table 3. Body weights in different experimental groups at 21 and 28 day-old chickens

Age		Control Neg	Non challenged		Challenged		Challenge control
			Bursaplex	Interm./Interm. plus	Bursaplex- CH	Interm./Interm. Plus-CH	
21 days	Mean	128.86	131.89	126.87	124.35	123.12	122.68
	SD	9.07	19.17	13.60	8.40	13.03	12.85
28 days	Mean	175.93	157.94	158.06	157.30	162.84	144.84
	SD	35.61	15.37	8.10	15.72	10.77	5.88

Table 4. Very virulent and vaccinal IBDV shedding detection at 28 day-old in vaccinated and vaccinated-challenged groups

Group	Sample	IBDV virus detection by RT-PCR		
		Very virulent IBDV	Vaccinal IBDV	Result
Bursaplex	5 pooled (bursa)	-	28,6	vvIBDV: NEG vacc.IBDV: POS
Interm./Interm. plus		-	24,3	vvIBDV: NEG vacc.IBDV: POS
Bursaplex- CH		-	30,8	vvIBDV: NEG vacc.IBDV: POS
Interm./Interm. Plus-CH		24,0	-	vvIBDV: POS vacc.IBDV: NEG
Challenge Control		25,6	-	vvIBDV: POS vacc.IBDV: NEG
Negative control		-	-	IBDV: NEG

DISCUSSION

In this study 2 vaccination schedules against vvIBDV were compared. Two live attenuated intermediate and intermediate plus vaccines at 9 and 14th day-old, respectively versus an immune-complex vaccine (Bursaplex) at day-old. The performance, bursal gross lesions, antibody immune response, and bursal histopathology were evaluated in vaccinated non challenged and vaccinated challenged birds. All vaccinated groups were protected against the vvIBDV challenge compared to 40% mortality in the challenge control group. Though the challenge control showed lower body weight, however, these differences were not statistically significant.

Both the immune-complex and live attenuated IBD vaccine groups showed higher BB ratios compared to the negative control group. However, on the 28th day of age, the BB ratio in the immune-complex vaccinated challenged group was significantly lower than the live attenuated group. Immune-complex IBDV vaccines have shown lower BB ratios especially when administered via in-ovo vaccination compared to live vaccine (Le Gros et al., 2009; Roh et al., 2016). Though intermediate plus vaccines contain more pathogenic strains (Sedeik et al., 2019), however, the BB ratios did not significantly differ from those of the immune-complex vaccine that might be attributed to the use of 2 doses of intermediate vaccine on the 9th day (Roh et al., 2016), and the intermediate plus vaccine at 14th day allowing for better bursal recovery than using intermediate plus vaccine alone (Aihara et al., 2015; Lupini et al., 2020).

Serologically, the ELISA antibody titers follow up in vaccinated non challenged groups indicated that Bursaplex vaccinated groups antibody titers were significantly higher except at 28th day of age, where the live attenuated vaccine was significantly higher. Similar results were previously reported (Zorman Rojs et al., 2011), where using an ELISA kit utilizing a bursa-derived antigen (e.g. Proflok plus IBD Ab kit, Synbiotics). After the challenge, the intermediate/intermediate plus vaccinated challenged group has significantly higher antibody titers at 21st and 35th days of age indicating more challenge virus replication compared to the immune-complex group (Abaza et al., 2020). These results were confirmed by the challenge virus detection and quantification on the 28th day where the vvIBDV was detected with high cycle thresholds (ct) value using the real-time RT-PCR indicating high shedding titers of the challenge virus (Techera et al., 2019). Conversely, a recent study showed that both immune-complex and live attenuated IBD vaccines did not induce sterile immunity as the challenge virus was detected in both groups (Ivanet al., 2005; Prandiniet al., 2016).

The immune-complex vaccinated challenged group developed milder bursal histopathology but the difference to the intermediate/intermediate plus vaccination regime was not significant. Previously, IBD live-vaccinated birds

displayed comparable histopathology to the challenge control group (Prandini et al., 2016; Kurukulasuriya et al., 2017), however, the alleviated bursal damage in the intermediate/intermediate plus vaccinated group may be attributed to the adjacent dosing regimen followed in the current study (i.e. 9th and 14th day of age). It is worthy to note that the current study was conducted in specific pathogen free chickens in the absence of maternally derived antibodies. Previous studies have shown that the immunocomplex vaccine showed poor immune response with even negative ELISA titers at 3 weeks of age due to the remaining neutralization antibody activity of the vaccine (Bose et al., 2016; Sedeik et al., 2019).

In conclusion, the use of either immune-complex vaccine at day-old or early vaccination with intermediate and intermediate plus live attenuated IBD vaccines induced protective antibody titers and both programs were clinically protective against an early vvIBDV challenge. However, the immune-complex vaccine induced sterile immunity as the challenge virus was not detected on the 28th day of age. Similar programs testing in commercial broilers in the presence of maternal derived IBD antibodies to simulate field conditions are required.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 565-570, December 25, 2020

Research Paper, PII: S2322455X2000064-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.64

Reproductive Performance of Koekoek Chickens at Different Levels of Feed Restrictions

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Received: 07 Oct. 2020
Accepted: 18 Dec. 2020

ABSTRACT

The objective of the present study was to determine the impact of the feeding levels on the reproductive characteristics of Koekoek chickens. A total of 270 Koekoek chickens were randomly assigned to 4 feeding level treatments in a completely randomized design. The four feeding level treatments were fully fed during the rearing and laying phase (AA), fully fed during the rearing phase and restricted feeding during the laying phase (AR), restricted feeding during the rearing phase and fully fed during the laying phase (RA), and restricted both during the rearing and laying phase (RR). The General Linear Model procedure (SPSS software, version 17) was used to analyze the data set. The pubic bone measurements were 23.6, 25.1, 16.1, and 15.1 mm for chickens that received AA, AR, RA, and RR treatments, respectively, at 18 weeks of age. At 32 weeks of age, chickens given AA and RA treatments had wider pubic bones than chickens given AR and RR treatments. Combined ova and oviduct weights were higher in the fully fed chickens at 18 weeks of age. Koekoek chickens in AA treatment had the highest average egg production. Chickens given AR treatment had lower average egg weights than those given AA, AR, and RR treatments. Chickens treated with AA and AR reached puberty earlier than those that were treated with the RA and RR treatments. The eggs produced by chickens given RR treatment had a higher average hatching percentage. The lowest percentage of hatches was observed in chickens that were fed *ad libitum* during the rearing phase. In conclusion, the feed restriction only during the rearing phase improved the reproduction performance of Koekoek chickens.

Keywords: Egg weight, Fully fed, Hatchability, Koekoek, Laying percentage, Oviduct, Pubic bone, Restricted

INTRODUCTION

Feeding is one of the greatest determinants required for higher egg production. The high costs of chicken feed are making it impossible for the poor resource farmers in rural areas of Lesotho to keep laying chickens. One of the strategies to reduce high feeding costs is to use restricted feeding**.** Salih et al. (2016) believed that periodic restriction of the daily feed to simulate compensatory growth was a means of reducing feed cost. Feed restriction was used to control the development of chickens in order to reduce the incidence of metabolic diseases and enhance feed efficiency (Trocino et al., 2020). In addition, Adegbenro et al. (2020) indicated that feed restriction was the strategy aimed at reducing the growth and metabolic rate and hence the delay in sexual maturity of chickens during the growing phase. This consequently increased body weight and production without negatively impacting welfare and health. Moreover, Simeneh (2019) confirmed that unrestricted feeding of laying hens led to waste of energy, which promoted the unnecessary build-up of abdominal fat and predisposed layers to heat stress.

Yildiz et al. (2006) considered feed restriction as a strategy to reduce oviduct development. Crounch et al. (2002) also reported that feed restriction during the rearing phase could result in heavier mature ova. The higher hatchability was recorded in the treatment with restricted feed in a study on turkeys (Crounch et al., 2002). However, Melnychuk et al. (2004) reported heavy oviducts in chickens that were fed *ad libitum*. Crounch et al. (2002) also found similar results although the study was performed on turkeys. Regarding ovary development, some studies indicated a greater weight in the *ad libitum* fed chickens (Melnychuk et al., 2004; Renema et al., 1999). On the other hand, the obtained results of a study performed by Evrim and Kaya (2014) showed similar laying production between quails fed differently prior to sexual maturity. In a study conducted on quails, it was indicated that fertility and hatchability were not affected by the feeding regime (Evrim and Kaya, 2014).

To cite this paper: Molapo Motsoene S, Webb E, Aloycia Mahlehla M, Chabeli Th, and Kompi P (2020). Reproductive Performance of Koekoek Chickens at Different Levels of Feed Restrictions. *J. World Poult. Res.*, 10 (4): 565-570. DOI: https://dx.doi.org/10.36380/jwpr.2020.64

Since the Koekoek chickens were introduced in Lesotho, insufficient or no scientific studies have been conducted on their feeding management. Therefore, it is important to determine the feeding level that aims to maximize egg production and hatchability at affordable feed costs. The present study was, therefore, carried out to investigate the effect of restricted feeding on the laying and hatching performance of Koekoek chickens.

MATERIALS AND METHODS

Ethical approval

The Research and Ethics Committee in the Department of Animal Science at the National University of Lesotho approved this study based on international animal welfare standards for the use of animals in conducting research.

Animals management and experimental design

The present study was carried out at the National University of Lesotho situated in Roma, Lesotho, an experimental farm of the Faculty of Agriculture. Chickens were bought and fed commercial feeds at eight weeks of age. Upon arrival, they were given a stresspack (water soluble vitamin and electrolyte supplement) to reduce travel stress, which could lead to death. Chickens were reared under the deep litter system. Each pen was equipped with three wooden nests measuring 40×40×40 cm. From 8 to 18 weeks chickens ate pullet grower, then from 19 to 32 weeks, they were fed laying mash bought from the local commercial feed manufacturer. Chickens were given water without restriction. A completely randomized design of four feeding level treatments was used. The four feeding level treatments were AA, AR, RA, and RR. Each treatment had 10 hens and one rooster. Each treatment was replicated 7 times, except for the RR treatment, which was replicated 6 times, which means there were 270 hens and 27 roosters. At day 130 and 32 weeks (224 days) of age, 7 Koekoek hens per treatment were killed by cervical dislocation. The chickens were starved for 24 hours prior to slaughter. The ovaries and oviducts were collected and weighed. The oviducts were emptied of the contents. The ovaries were examined for follicular development. The diameter of the pubic bones was measured. The eggs were collected daily and an average laying percentage was calculated for each week throughout the study period. The egg weights were recorded after 25 weeks, at which the majority of chickens began to lay in all replicates. The ages at which Koekoek chickens first reached puberty (point of lay), 20%, 50%, and greater or equal to 80% egg productions were recorded. A sample of three eggs weighing between 50 and 55 gram (g) from each replicate for all treatments and less than eight days old was removed and placed in a model SH680 fully automatic digital egg incubator made in South Africa. During the incubation period, the eggs were not turned for the first three days. During days 4-18, egg turning was done three times a day. On day 18, the eggs were removed from trays and placed into the hatching trays until hatching time. The incubator was not disturbed for the last three days of incubation. The chickens were removed from the incubator in the morning after 22 days. The hatching percentage of the eggs was calculated as follows:

Hatching percent = Total number of eggs hatched × 100 / Total number of eggs incubated

Statistical analysis

The data were analyzed using the statistical package for social sciences (SPSS version 17). General Linear Model (GLM) procedure was used to analyze the effect of feed restriction on the reproductive performance of Koekoek chickens.

RESULTS

Ova and oviducts weights

The weight of the ova and oviduct in pullets fully fed during the rearing phase (AA and AR) was 64.6% higher than that in the restricted feeding treatments (RA and RR) as stated in table 1. At 32 weeks of age, Koekoek hens that were fed unrestrictedly during the laying phase (AA and RA) had similar ($p<0.05$) ova weights, compared to those that were fed restrictedly during the laying phase (AR and RR). Despite the insignificant differences in ova weight between chickens that were subjected to different feeding levels, the ova weights of restricted feeding chickens (RR) were higher ($p>0.05$) than those of hens that were in the AA, AR, and RA treatments by 3.4%, 2.5%, and 4.7%, respectively. This suggests that restricted feeding during the laying phase stimulated the ova production in Koekoek chickens.

Pubic bones width

At puberty (18 weeks), fully fed Koekoek chickens had higher ($p<0.05$) pubic bone measurements than those under feed restriction (Table 1). On average, the pubic bone widths of chickens that were fully fed were 35.9% greater ($p<0.05$) than the average pubic bone widths of chickens that were subjected to restricted feeding at 18

weeks of age. During the laying phase (32 weeks), Koekoek chickens that were fully fed during the laying phase had larger ($p<0.05$) pubic bone widths than those that were fed restrictedly. Koekoek chickens in the RA treatment had a faster pubic bone width growth of 66.9%, followed by chickens in the RR treatment with 66.2%. The lowest in pubic bone width growth was observed in chickens assigned to the AR treatment (40.5%), while chickens assigned the AA treatment (51.8%) ranked the third position between 18 and 32 weeks. These results revealed that restricted feeding during the rearing phase promoted the development of the pubic bones more than full feeding during the same period.

Table 1. Pubic bones, ova, and oviduct growth of Koekoek chickens subjected to different levels of feeding treatments

		Treatments				
Age	**Variables**	**AA**	**AR**	**RA**	**RR**	**S.E**
18 weeks	Pubic bone (mm)	23.6[a]	25.1[a]	16.1[b]	15.1[b]	0.66
	Ova and oviducts (g)	16.0[a]	15.4[a]	5.5[b]	5.5[b]	0.39
32 weeks	Pubic bone (mm)	48.9[a]	43.9[b]	48.8[a]	44.6[b]	0.50
	Ova weight (g)	46.1	46.6	45.5	47.8	0.78
	Oviduct weight (g)	49.1	48.1	52.0	48.0	0.80

[a,b:] Means within a row with no common superscript differ significantly ($p<0.05$), S.E: Standard Error. AA: Full feeding during rearing and laying, AR: Full feeding during rearing and restricted during laying, RA: Restricted feeding during rearing and full feeding during laying, RR: Restricted feeding during rearing and laying.

Laying performance

Koekoek chickens that were subjected to different feeding levels had ($p<0.05$) different laying percentages between 18 and 32 weeks of age (Figure 1). Koekoek chickens that were fully fed during the rearing phase (AA and AR) had a significantly ($p<0.05$) higher laying percentage between 19 and 21 weeks old, compared to those with restricted feeding (RA and RR). Koekoek chickens that were fully fed throughout the study (AA) had the highest laying percentage, followed by those that were only fed restrictedly during the rearing phase (RA). Koekoek chickens that were only fed restrictedly during the rearing phase (RA) responded positively to the fully fed diet after four weeks. The positive response of RA treatment can be confirmed by the similar laying percentages of chickens that were in the AA and RA treatments from week 25. On average, chickens that were fully fed during the rearing and laying phase (AA) had higher ($p<0.05$) laying percentage.

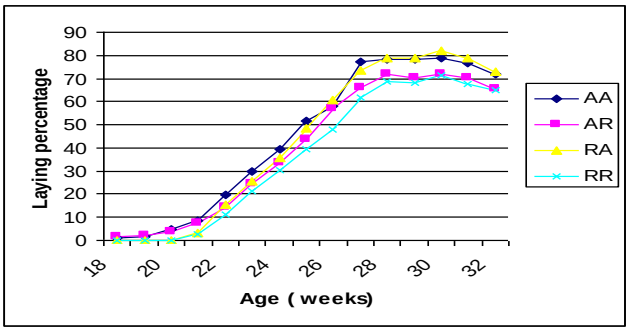

Figure 1. The laying percentage of Koekoek chickens subjected to different feeding levels. AA: Full feeding during rearing and laying, AR: Full feeding during rearing and restricted during laying, RA: Restricted feeding during rearing and full feeding during laying, RR: Restricted during rearing and laying,

Egg weights

The egg weight of chickens that received different feeding level treatments significantly differed ($p<0.05$) throughout the experiment, except at the ages of 27 and 28 weeks (Table 2). At 25 weeks of age, the egg weights of Koekoek chickens that were fed restrictedly for the entire study (RR) were 27.4%, 22.6%, and 30.4% lower ($p<0.05$) than the egg weights of chickens that were under the AA, RA, and AR treatments, respectively. On average, chickens that were fully fed during the laying phase (AA and RA) produced eggs of higher weights ($p<0.05$) than those that were exposed to restricted feeding (AR and RR) during the same phase.

Different egg production stages

The results on how chickens that were either full-fed or restricted fed performed in terms of age at puberty, 20%, 50%, and 80% egg production are presented in table 3. The results revealed that restricted feeding affected the number of days to reach different egg production phases.

Hatchability

Eggs produced by Koekoek chickens subjected to feed restrictions during the laying period (AR and RR) hatched higher ($p<0.05$) than the eggs from chickens that were unrestrictedly fed during the laying phase (AA and RA) at 28 weeks of age (Table 4). Restricted feeding during the laying phase increased the hatchability of the eggs in Koekoek chickens. The hatching percentages of eggs in the RR treatment were 13.5%, 8.9%, and 10.5% higher ($p<0.05$) than in chickens assigned to the AA, AR,

and RA treatments, respectively. Hatchability increased with age since the hatching percentages of eggs produced from chickens under the AA, AR, RA, and RR treatments increased by 23%, 10.9%, 21.4%, and 8.9%, respectively. Generally, restricting feed during the laying period could increase hatchability, compared to feeding completely during the laying phase. This meant that the hatching percentage during the laying phase is negatively related to the feed intake and body weight of chickens.

Table 2. Egg weights of Koekoek chickens subjected to different feeding level treatments

Treatments / Age (Weeks)	AA	AR	RA	RR	S.E
25	37.5^{a}	35.6^{a}	39.6^{a}	27.6^{b}	1.06
26	45.5^{a}	39.7^{b}	45.0^{a}	39.0^{b}	0.73
27	46.3	45.7	47.2	46.9	0.32
28	46.0	45.0	47.1	46.9	0.42
29	48.4^{a}	46.3^{b}	48.1^{a}	46.7^{ab}	0.27
30	47.9^{ab}	47.3^{a}	49.2^{b}	48.1^{ab}	0.29
31	48.0^{a}	46.3^{b}	49.2^{a}	47.5^{ab}	0.29
32	49.2^{a}	43.9^{b}	50.2^{a}	46.9^{b}	0.70
Average	45.6^{a}	43.5^{b}	46.7^{a}	43.1^{b}	0.22

$^{a, b, c:}$ Means within a row with no common superscript differ significantly ($p<0.05$), S.E: Standard Error; AA: Full feeding during rearing and laying, AR: Full feeding during rearing and restricted during laying, RA: Restricted feeding during rearing and full feeding during laying, RR: Restricted feeding during rearing and laying.

Table 3. The number of days it takes Koekoek chickens to reach the first oviposition, 20%, 50%, and greater or equal to 80% egg-laying production

Treatments / Variables	AA	AR	RA	RR	S.E
Number of days to 1st oviposition	150.1^{a}	152.4^{a}	159.0^{b}	159.8^{b}	0.61
Number of days to 20% production	163.5^{a}	164.1^{b}	166.9^{ab}	168.3^{b}	0.79
Number of days to 50% production	174.1	172.8	175.0	176.1	0.79
Number of days to ≥ 80 % production	191.7^{a}	190.7^{a}	189.1^{a}	199.4^{b}	1.19

$^{a, b:}$ Means within a row with no common superscripts differ significantly ($p<0.05$). S.E: standard error; AA: Full feeding during rearing and laying, AR: Full feeding during rearing and restricted during laying, RA: Restricted feeding during rearing and full feeding during laying, RR: Restricted feeding during rearing and laying

Table 4. Egg hatching percentage of Koekoek chickens subjected to different feeding levels

Treatments / Age (Weeks)	AA	AR	RA	RR
28	62.1^{a}	75.7^{b}	65.7^{a}	85.0^{b}
30	75.0^{a}	89.3^{b}	78.6^{a}	92.5^{b}
32	80.7^{a}	85.0^{a}	83.6^{a}	93.3^{b}
Average	72.6^{a}	83.3^{b}	76.0^{a}	90.3^{c}

$^{a, b, c:}$ Means within a row with no common superscript differ significantly ($p<0.05$). AA: Full feeding during rearing and laying, AR: Full feeding during rearing and restricted during laying, RA: Restricted feeding during rearing and full feeding during laying, RR: Restricted feeding during rearing and laying, S.E: Standard Error

DISCUSSION

Concerning the ova weights, the results of the present study agreed with the findings of Crounch et al. (2002), who stated that the maturing ova were heavier in turkeys that were fed restrictedly during the rearing period than in those that were fed *ad libitum* in the rearing phase. Simeneh (2019) also found that limited feed at the rearing phase hindered the development of the oviducts. On the contrary, Renema et al. (1999) pointed out that restricted feeding chickens were 38% lower than *ad libitum* feeding chickens in terms of the ovary weights. In addition, Robinson et al. (2007) reported that the ovary weights were influenced by body weight and possibly by fat content. Yildiz et al. (2006) also suggested that *ad libitum*-fed chickens showed accelerated development of oviducts.

The findings of previous researchers indicated similar oviduct weights between chickens that were

subjected to different feeding regimes at sexual maturity (Tesfaye et al., 2009; Renema et al., 2007; Renema et al., 1999). Yildiz et al. (2006) also suggested that restricting feed during the rearing period significantly delayed oviduct development. Moreover, Cassy et al. (2004) and Renema et al. (2007) confirmed that chickens that were exposed to feeding restrictions during the growing period had a decreased number of large yellow follicles at first oviposition.

Crounch et al. (2002) also found that the total egg production was higher in chickens that were fully fed during the laying period. The findings of the present study tally with the results of Oyedeji et al. (2007) who reported that the egg weight was significantly higher in hens that were fed *ad libitum*, compared to those that were restricted.

Concerning egg weight, Moreira et al. (2012) also stated that it was not affected by the dietary restriction. Evrim and Kaya (2014) also found that early feed restriction did not affect the average egg weights in quails. On the other hand, Miles and Jacqueline (2000) showed that a feed restriction program would result in a slight decrease in egg size, which was less significant when the majority of eggs were in large category, which was in line with the results of the present study showing the effect after 30 weeks.

It was found that the reduction of egg production in layers that were restrictedly fed throughout the study (RR), the last group to reach one of the egg production stages, was consistent with the obtained results of a study conducted by Ezieshi et al. (2003). In a study on quails, Evrim and Kaya (2014) emphasized that feed restriction delayed the onset of laying as was observed in the findings of the present study since chickens treated with feed restrictions during the rearing phase (RA and RR) experienced delayed sexual maturity. In addition, Onagbesan et al. (2006) stated that chickens with restricted feeding would take a longer period to reach maximum egg production than chickens that were fully fed. Crounch et al. (2002) also stated that turkeys that were fed restrictedly at the rearing period (3-16 weeks) had a significantly higher egg production than those that were fully fed during the growing period.

In support of these results, Simeneh (2019) stated that early feed restriction reduced overall embryonic mortality. Crounch et al. (2002) also indicated that turkeys that were shifted from restricted feeding during the rearing phase to *ad libitum* feeding during the laying phase had a significantly higher embryonic mortality, and thus a lower hatching percentage compared to the other treatments. Evrim and Kaya (2014) also reported that mortality in fully fed quails increased by 56%.

CONCLUSION

Full feeding during the rearing phase resulted in reduced pubic bones, ova, and oviducts development, delayed oviposition, and 20% egg production. Full feeding in the laying phase led to a higher laying percentage and egg weights despite the fully fed or restrictedly fed diets of chickens during the rearing phase. Therefore, Koekoek chickens should only be fed restrictedly during the rearing phase since their performance in terms of laying percentage, egg weight, and early peak egg production did not differ from those that were fully fed throughout the study. In the case where a farmer is interested in hatching, a feed restriction would be an ideal practice in order to maximize egg hatchability.

DECLARATIONS

Acknowledgements

The authors would like to thank the Department of Animal Science of the National University of Lesotho for providing facilities used in the current study.

Competing interests

The authors declare that they have no conflict of interest.

Author's contribution

Setsumi M. Molapo and Edward Webb developed the concept, analysed data and wrote the manuscript. Motselisi A. Mahlehla and Paseka Kompi assisted in data collection while Thato Chabeli designed the graphical abstract. All authors reviewed and confirmed the manuscript before submission.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 571-579, December 25, 2020

Review Paper, PII: S2322455X2000065-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.65

Phytobiotics in Poultry Industry as Growth Promoters, Antimicrobials and Immunomodulators – A Review

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Received: 02 Nov. 2020
Accepted: 20 Dec. 2020

ABSTRACT

Due to the hazardous use of antimicrobials in poultry production sector, development of drug resistance have become a worldwide problem. Therefore, using biotic or natural products, such as phytobiotics (phytogenics or botanicals) have received a great attention as antibiotic substitutes. The use of phytobiotics or their constituents have been considered as a relatively new class of natural herbs that gained popularity and acceptability among poultry farmers. The incorporation of several types of phytobiotic additives in poultry feed have proved their ability to enhance the productive performance of broilers as well as layers. Moreover, phytbiotics presented great efficacy in counteracting intestinal pathogenic microorganism while maintaining the population of normal inhabitant beneficial microflora. Immunostimulatory effect on both humoral and cellular immunity as well as antioxidant properties were recorded as characters of phytobiotics. Therefore, this review article aimed to give a spotlight on the uses of different types of phytobiotics as poultry dietary additives to improve the productive parameters, reduce the pathogenic intestinal bacteria, and potentiate the immune response, especially after vaccination processes.

Keywords: Antimicrobial, Immunity, Performance, Plants, Poultry

INTRODUCTION

From several decades till now, poultry industry has been recognized as an important subsector of agricultural and veterinary fields due to increasing demand for meat and eggs as low cost protein sources. Continues feeding by sub-therapeutic levels of antimicrobials as growth promoter agents or antimicrobial compounds have had a negative impact on the balance of normal inhabitants of gut microflora, accumulation of antibiotic tissues residues as well as developing new strains of drug-resistant pathogenic bacteria (Castanon, 2007). Therefore, in 2006, the European Union Commission banned using of antibiotics in animal feeds as a growth promoter in different countries (Europe Union Commission, 2005).

Phytobiotics are also termed as phytogenics or botanicals. They are defined as natural, less toxic, and residue free plant-derived compounds that have been used as feed additives for livestock production (Wang et al., 2008). Phytobiotics are composed of natural bioactive components or substances of plant origin including terpenoids, alkaloids, glycosides and phenolics (Shad et al., 2014). Phytobiotics could be classified as herbs from flowering, non-woody and non-persistent plants, botanicals or spices from non-leaf parts like seeds, fruits, bark or root, essential oils or extracts and oleoresins (Bote, 2004).

Numerous studies have been conducted to demonstrate the effect of phytobiotics as growth promoter feed additives like prebiotics and probiotics to enhance overall performance parameters as well as health conditions of poultry (Yasodha et al., 2019; Özbudak, 2019). Phytobiotics have been also used as antimicrobial, antiparasitic, anticoccidial as well as immunostimulant agents in poultry field (Manafi, 2015; Gilani et al., 2018; Hafeez et al., 2020). Phytogenic substances were extremely studied in different species of monogastrics (Gheisar and Kim, 2018), rabbits (Alagawany et al., 2018; Al-Sagheer et al., 2019) and fish (Naiel et al., 2019).

So, the purpose of current article review was to spotlight on phytogenic compounds that used in poultry field and their effects on the productive performance, antimicrobial activities and immuno-stimulatory properties.

Production parameters

Improved growth parameters were detected in birds fed on different kinds of herbs, polysaccharides or essential oils components (Yasodha et al., 2019). The enhancement of the growth performance parameters after supplementation of phytobiotics may be depends on the synergistic mechanism among their active molecular complex (Hussein et al., 2020a). Phytobiotics could maintain or improve normal intestinal architecture, increase the villus length and consequently increase the surface of intestinal absorption (Tabatabaei, 2016). It has been demonstrated that phytobiotics are able to stimulate saliva production, secretion of digestible enzymes and bile production resulting in improving the performance and digestibility (Alloui et al., 2014). Moreover, phytobiotics enhance the digestion and digestion and utilization of protein in the intestine (El-Gendi, 1996), decrease the gut pathogens (Kubkomawa et al., 2013) and increase *Lactobacillus* spp. count (Windisch et al., 2008). It has been observed that supplementation with herbal feed additives can alter the histological structure of the intestine and indicated elevation of the intestinal villi by deepening of its crypts (Murali et al., 2012), increasing the dendritic cells absorption capacity in the intestinal lumen, stimulation of toll-like receptors and activation of epithelial to release the mucosal cytokines. Alcicek et al. (2004) assumed that feeding of broilers on phytobiotics stimulated the secretion of high amount of intestinal mucus and consequently reducing the pathogens adhesion and establishment of gut microbial eubiosis.

Supplementing broiler feed or water with essential oil mixtures of thymol and cinnamaldehyde (Tiihonen et al., 2010), thymol and star anise (Kim et al., 2016), clove and cinnamaldehyde (Chalghoumi et al., 2013), coriander (Ghazanfari et al., 2015; Hady et al., 2016), oregano (Hashemipour et al., 2014), a mixture of oregano, anise, and citrus peel (Abdelnaser et al., 2019), carvacrol (Jamroz et al., 2006), a blend of carvacrol, cinnamaldehyde and capsicum oleoresin (Bravo and Ionescu, 2008) and ginger extract (Olaifa et al., 2019) had been detected for improving all performance parameters including; feed intake, feed conversion rate and body weight. Moreover, supplementation of broilers diet with garlic (Elagib et al., 2013), a mixture of garlic, mushroom and propolis (Daneshmand et al., 2012), turmeric powder (Ahmadi, 2010), guggul resin (Iranparast et al., 2014), dried ground leaves of stevia (Atteh et al., 2008) and black cumin seeds (Khalaji et al., 2011) presented the enhancement of broilers performance. Studies on the effects of herbal compounds on the production of broilers Japanese quail's revealed improvement of all performances (Manafi et al., 2016).

The laying hens represented improvement in egg production, eggshell strength and thickness as well as internal egg quality after treatment with mixture of plant extracts and essential oils (Bölükbaşi et al., 2008; Radwan et al., 2008; Kaya et al., 2013).

Antimicrobial effect

It has been demonstrated that phytochemical compounds of phytobiotics have a strong antimicrobial activity against Gram-positive and Gram-negative bacteria either *in vivo* (Al-Kassie, 2010; Daka, 2013) or *in vitro* environment (Al-Mariri and Safi, 2014). Some phytochemical compounds as alkaloid inhibit DNA synthesis (Karou et al., 2005) and form saponin complexes with the cell membrane (sterols) which leading to cells damage and collapse (Morrissey and Osbourn, 1999). The antimicrobial effect of essential oils could be refer their ability to penetrate through the bacterial membrane (Helander et al., 1998), their chemical structure (Farag et al., 1989) and their aromaticity (Bowles and Miller, 1993).

Modulation of the gut microflora by phytogenic compounds plays an important role in maintaining host health (Tollba et al., 2012). Several studies revealed that phytogenic compounds or their extracts reduce the population of intestinal pathogenic organisms and their metabolites, but increase the number of intestinal normal and helpful microflora which relief the intestinal challenge and immune stress and consequently increase intestinal performance (Liu et al., 2014). It has been speculated that organic acids of some phytobiotic feed additives may lower the intestinal pH that leaded to inhibiting the pathogenicity of local pathogens and lowering the level of their toxic products (Manafi et al., 2016).

Antibacterial effect

Essential oils could reduce the growth of common intestinal poultry pathogens. Inoculation of thyme and cinnamon in the broiler ration reduces the total bacterial as well as coliform count in the intestinal tract (Karangiya et al., 2016). An *in vitro* study revealed that flowers of Calendula presented growth inhibitory effects on *Escherichia coli* (*E. coli*) (Arora et al., 2013). However, some reports indicated the inhibitory effects of dietary phytobiotics or plant extracts on *E. coli* activity *in vivo* (Abd El-Ghany and Ismail, 2014; Diaz-Sanchez et al., 2015; Elmenawey et al., 2019). Diet containing thyme essential oil helped for increasing in *Lactobacillus* and decreasing in *E. coli* counts in the intestine of Japanese

quail (Khaksar et al., 2012). Essential oils of oregano revealed antimicrobial properties on broiler carcasses through reduction of the total bacterial count especially *Salmonella* spp. (Aksit et al., 2006). Short chain fatty acids of phytobiotics revealed growth promoting effect on the intestinal beneficial microbiota as well as controlling the growth of *Salmonella enteritidis* (*S. enteritids*) (Hansen et al., 1997). Quail's diet containing phytobiotic feed additives had significant (P≤0.05) increase in the number of *Lactobacilli*, decrease in *E. coli* population and inhibit the growth of *Salmonella* in the intestinal tract (Dorman and Deans, 2000).

The efficacy of a mixture of seven essential oils that inhibited the growth of *Clostridium perfringens* (*C. perfringens*) *in vitro* has been reported by Si et al. (2009). In the field studies of Mitsch et al. (2004), Siragusa et al. (2008), McReynolds et al. (2009), Abudabos et al. (2018), El-Sheikh et al. (2018) and Hussein et al. (2020b), different phytobiotic feed additives caused reduction of intestinal colonization and proliferation of *C. perfringens*, lesion score and mortalities as well as improvement in performance of broilers and their carcass quality.

The reduction in *C. perfringens* virulence after supplementation with essential oil compounds may be related to the stimulation of some digestible enzymes like trypsin which inactivates α toxin of type A and β toxin of type C strains of *C. perfringens*, stabilization of natural resident gut microflora like *Lactobacillus* spp. and consequently inhibition of the organism pathogenicity (Cho et al., 2014).

Moreover, essential oils of lemon, green tea and turmeric blend proved great efficacy in reducing the count of *S. enteritidis* and *Campylobacter jejuni* on the surface of chicken's carcass (Murali et al., 2012). The Eucalyptus volatile oils have been found to have the ability to relief broilers complicated respiratory distress caused by Mycoplasma gallisepticum (Abd El-Ghany, 2008).

Antifungal and detoxifying effect

Phytogenic compound have antifungal properties. Akgul and Kivanc (1988) reported about the inhibitory effects of some spices and oregano components on some foodborne fungi. Essential oil of marjoram reduced the *in vitro* growth of *Aspergillus flavus*, *A. niger*, *A. ochraceus* and *A. parasiticus* up to 89% (Deans and Waterman, 1993). The oil of lemon and orange can reduce the formation of *A. flavus* (Hasan et al., 2005). It has been demonstrated that *Allium sativum* has a great (60-80%) *in vitro* antifungal activity against *Aspergillus* and *Penicillium* spp. (Afzal et al., 2010). Onion, garlic and ginger revealed antifungal activity against *A. flavus*, *A. niger* and *Cladosporium herbaru*, *Cinnamomum verum* and *Piper nigrum* which was studied with successful results by Tagoe et al. (2011). Phytobiotics *like Ocimum gratissimum, Cymbopogon citratus, Xylopia aethiopica, Monodora myristica*, *Syzygium aromaticum* proved their ability to inhibit the formation of non sorbic acid which is a precursor in the pathway of aflatoxin synthesis (Awuah, 1996). Neem extract represented inhibitory effects on biosynthesis of aflatoxins (B and G) (Bhatnagar et al., 1990). Also, neem leaf extract and its oil have been found to inhibit the growth and morphology of *Penicillium* spp. and consequently prevent the production of ochratoxin A (Bhatnagar et al., 1990).

Anticoccidial effect

The anticoccidial activity of some herbal plants have been documented (Willis et al., 2013). Phytogenic compounds have been found to reduce the severity of *Eimeria* spp. infection in broilers by alleviation of droppings score, intestinal lesions score and also reducing oocyst shedding (Zyan et al., 2017). Numerous phytobiotics as Atemesia annua (Allen et al., 1997), *Astragulus membranaceus* and *Sophora flavescens* (Youn and Noh, 2001), green tea (Jang et al., 2007), *Ageratum conyzoid* (Nweze and Obiwulu, 2009), *Musa paradisiaca* (Anosa and Okoro, 2010), olive tree (De Pablos et al., 2010), oregano essential oil (Tsinas et al., 2011), *Carica papaya* leaf extract (Nghonjuyi et al., 2015) and coconut oil (Hafeez et al., 2020) have indicated an excellent anticoccidial activity against different types of *Eimeria* spp. in birds.

Some essential oils presented similar drug efficacy in prevention and control of coccidiosis in broilers. The oregano oil and other mixtures of oils were similar to ionophores lasalocid (Giannenas et al., 2003) and monensin (Oviedo-Rondón et al., 2006), while a mixture of carvacrol, camphor, cineole and thymol was similar to salinomycin (Bozkurt et al., 2014) in terms of reduction of shedding and lesions of different *Eimeria* spp. in broilers.

Combined experimental infection of *C. perfringens* and *E. maxima* has been ameliorated after dietary treatment of three breeds of broilers with Capsicum, Curcuma longa oleoresins (Kim et al., 2015) and Allium hookeri root (Lee et al., 2018).

Immunomodulatory effect

In poultry production, reduction of infection as well as improvement of production by stimulation of the immune system after using phytogenic substances were

investigated previously (Zaki et al., 2016). The immunomodulatory mechanism of phytogenic active substances in poultry have been studied (Hashemi and Davoodi, 2012). Polysaccharide are very important immunoactive components of phytobiotics (Xue and Meng, 1996). Phytogenic compounds also induce their immunomodulatory effects through increasing immune cells proliferation, arising cytokines expression and elevation of antibody titers (Lee et al., 2010; Park et al., 2011; Pourhossein et al., 2015). The immunogenicity of phytobiotics could be manifested as increasing macrophages, lymphocytes and natural killer cells activities as well as stimulation of interferon production (Hashemi and Davoodi, 2010; Kumar et al., 2014). Plants contain flavonoids, vitamin C and carotenoids are able to enhance the immune system (Craig, 1999). Some herbs and species like garlic, echinacea and liquoric have immunostimulatory properties due to their composition of vitamin C, carotenoids and flavonoids as well as their abilities to stimulate macrophages, lymphocytes and natural killer cells activities and interferon production (Frankic et al., 2009). Detecting *in vitro* immuno-stimulatory effect of dandelion, mustard and safflower either on lymphocytes and macrophages of chickens was performed by Lee et al. 2007. The results indicated inhibition of tumor cell growth, antioxidant effects, stimulation of lymphocyte proliferation and nitric oxide production by macrophages. The immunostimulant effect of some essential oils extracts of phytobiotics may be due to the presence of certain compounds that may bind to Immunoglobulin G (Ig G) receptors which leaded to stimulation of immune response (Ahmed et al., 2013). In the study of Placha et al. (2014), inoculation of thymol in the broiler diet increased the trans-epithelial electrical resistance of duodenal mucosa.

It has been found that mushroom and plant polysaccharides have immunomodulatory effects in chickens infested with *Eimeria tenella* (Guo et al., 2004).

Potential antiviral activity of plant seeds was recorded (Yaseen, 2003). Different types of herbs mix, spices, plant extracts and essential oils presented enhancement of immune response of birds (Huang et al., 2007; Pourali et al., 2010; Kavyani et al., 2012; Abou-Elkhair et al., 2014; Awaad et al., 2016).

A significant ($P<0.05$) elevation of antibody Enzyme-linked immunosorbent assay (ELISA) titer after vaccination with Newcastle Disease Virus (NDV) vaccine (Chowdhury et al., 2018) was recorded after feeding on clove bud and cinnamon plant, while peppermint essential oil helped in significant ($P<0.05$) rising in Haemagglutination Inhibition (HI) antibody titer against Avian Influenza (AI) virus vaccines (H9N2) in broiler chicks (Sultan et al., 2017). In addition, significant ($P<0.05$) increase in HI titers against NDV vaccine and sheep red blood cells were observed in broiler chicks treated with Aloe vera gel (1%) in the drinking water for six weeks (Darabighane et al., 2017)

Laying hens presented significant ($P>0.05$) increase in ELISA titer after vaccination with ND, Infectious Bronchitis (IB) and Infectious Bursal Disease (IBD) vaccines (Özek et al., 2011). Landy et al. (2011) observed that inoculation of broiler ration with neem powder for six weeks resulting in an elevation of HI antibody titer against AI vaccine, but not against ND vaccine. Barbour et al. (2008) evaluated the effect of using Eucalyptus and peppermint essential oils during vaccination of ND and IBD. The results indicated improved health conditions of the birds associated with elevation of ELISA titers against the used virus vaccines. Moreover, an increase in IgG and IgM ELISA titers has been observed in chickens fed on oregano essential oils for three weeks period (Malayoglu et al., 2010). Recently, Abdelnaser et al. (2019) indicated that treatment with essential oils of oregano, anise, and citrus peel at level of 125 gm/ton induced positive effects on the immune response of *C. perfringens* challenged broilers after vaccination against ND, IB, AI and IBD viruses as well as increasing in relative spleen weight.

CONCLUSION

Using of phytobiotics in poultry diet as a feed additive and considering them as an antimicrobial substitute has been became a very essential and critical issue currently. Phytobiotic compounds could replace antibiotic growth promoters to improve the productive performance of chickens, act as antibacterial, antifungal and antiparasitic agents as well as it has been considered as potential immunostimulants especially after routine vaccination programs of chickens. This review spotlight on the significant using of phytobiotics in poultry field and industry as natural antibiotic alternatives to avoid the emerged problem of antibiotic resistance,

Competing interests

The author have not declared any conflict of interest.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 580-586, December 25, 2020

Research Paper, PII: S2322455X2000066-10

DOI: https://dx.doi.org/10.36380/jwpr.2020.66

Phenotypic Correlations among Various Egg Quality Traits in Pearl Grey, Lavender, Royal Purple, and White Varieties of Helmeted Guinea Fowl

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Received: 15 Oct. 2020
Accepted: 03 Dec. 2020

ABSTRACT

Guinea fowls are increasingly popular in Botswana since they not only provide an alternative to access protein in the form of eggs and meat but also become a good source of income for the peasants. There are different varieties of Guinea fowl in Botswana, including pearl grey, lavender, royal purple, and white. Indeed, there is a need to conduct more studies related to the phenotypic correlations among egg quality traits in different varieties of helmeted guinea fowl found in Botswana. Therefore, the present study was targeted toward the evaluation of both the external and internal quality characteristics of the four different varieties of the domesticated helmeted guinea fowl found in Botswana. In this regard, a total of 150 eggs were collected from the so-called varieties of domesticated helmeted guinea fowl. The egg weight was positively and significantly correlated with egg length, egg width, shell weight, egg surface area, and egg volume; however, the egg weight was negatively correlated with egg shape index. Of the four varieties of domesticated helmeted guinea fowl found in Botswana, the white variety had the strongest correlation coefficients with various external egg quality traits and different internal egg quality characteristics. The lavender variety had the highest correlation coefficients with internal and external egg quality traits. It seems that the selection for higher egg weight as is the case in the current egg grading system can lead to the greatest improvements in other egg quality characteristics in the white and lavender varieties, compared to the pearl grey and royal purple varieties. Therefore, the lavender and white varieties are the potential candidates for the possible selection of layer-type guinea fowl varieties.

Keywords: Botswana, Egg traits, Guinea fowl, Layer-type

INTRODUCTION

Guinea fowl production in Botswana is still at its early developmental stage and presents a viable alternative for the diversification of the country's poultry sector (Kgwatalala et al., 2013). Guinea fowl production has great potential because guinea fowl meat is an acceptable food product and its consumption is not restricted by any traditional or religious taboos (Alkan et al., 2013). Some challenges facing guinea fowl production in Botswana include poor management skills by farmers, insufficient technical and financial support from government extension services (Moreki and Seabo, 2012). Guinea fowl provide an alternative for the rural population in Botswana to access protein in the form of meat and eggs and have great potential for revenue generation through sales of live birds and eggs (Kgwatalala et al., 2013). Guinea fowl production could be a viable alternative to failed commercial chicken enterprises in rural areas of Botswana since guinea fowls are tolerant of poultry diseases compared to chickens (Moreki and Seabo, 2012). In Africa, guinea fowl production is practiced on a small scale due to the poor performance of native genotypes, and lack of information regarding genetic and phenotypic differences in traits of economic (Alkan et al., 2013). Apart from guinea fowl meat, guinea fowls also produce eggs which are often sold hard-boiled in local markets in many African countries (Adeyeye, 2012) or as fresh eggs for artificial incubation and hatching. Understanding the structure of the egg and its various components is essential for understanding egg quality, egg fertility, embryo

development, and diseases of poultry (Islam and Duta, 2010). Phenotypic correlations among various egg quality characteristics are useful in predicting the consequences of selection for a particular trait on other traits of economic importance. It seems that currently there is very limited work on phenotypic correlations among various egg quality characteristics in different varieties of helmeted guinea fowl found in Botswana. The purpose of the current study was therefore to compute correlations among various egg quality traits in pearl grey, royal purple, white, and lavender varieties of helmeted guinea fowl found in Botswana.

MATERIALS AND METHODS

Location and duration of the study

The study was conducted at the Botswana University of Agriculture and Natural Resources (BUAN), Content Farm, Sebele, Gaborone, in the Southern part of Botswana. BUAN is located at 25.94^0S, 24.58^0E at an altitude of 991 meters. The study commenced at the beginning of January 2018 and ended in the middle of March 2018.

Housing and management

The samples in this study were divided into 30 females and 5 males of pearl grey variety, 30 females and 5 males of royal purple variety, 30 females and 5 males of the white variety, and finally 30 females and 5 males of lavender variety. The four varieties of guinea fowl were raised under an intensive management system in four separate deep litter houses with concrete floors covered with wood shavings. The four deep litter houses were of similar dimensions and measured 9m x 4m. The guinea fowls were fed commercial broiler grower pellets and provided with water *ad libitum* throughout the study period. The guinea fowl were of the same age and the egg collection began when guinea fowl were 25 months of age and lasted for 7 days. The guinea fowl were raised under natural light (12hr light and 12hr dark periods) throughout the study phase.

Collection of eggs

A total of 150 eggs were collected from each variety of domesticated helmeted guinea fowl for the evaluation of both external and internal egg quality characteristics. The guinea fowl providing the eggs were of the same age (25 months) and were hatched on the same day via artificial incubation.

Measurements of egg quality traits

The investigated external egg quality characteristics included egg weight (g), egg length (cm), egg width (cm), egg surface area (cm^3), shell thickness (mm), and egg shape index (%). The examined internal egg quality characteristics entailed yolk weight (g), yolk width (cm), yolk height (cm), fresh albumin weight (g), albumin index (%), albumin (%), yolk (%), and yolk index (%). Egg weight was determined using an electronic balance, while egg length and egg width were determined using an electronic vernier caliper. Eggshell thickness was determined using a micrometer screw gauge calibrated in mm. The accuracy of shell thickness was ensured by measuring shell thickness at the broad end, a middle portion, and narrow end of the shell and taking the average of the three measurements.

Statistical analysis

The different external and internal egg characteristics of various varieties of the helmeted guinea fowl were evaluated using correlation procedures of the Statistical Analysis System (SAS Institute Inc., Cary, NC, USA, SAS, 2010). The correlations procedure of SAS automatically tested for a significant association between various pairs of traits at $P \leq 0.05$.

Ethical approval

The rearing of the research birds was approved by the Animal Research Ethics Committee of the Botswana University of Agriculture and Natural Resources (Approval No. 2020-10), which conforms to the guidelines and the use of research animals.

RESULTS AND DISCUSSION

Phenotypic correlations among external egg quality traits

Significant positive correlations were observed between egg weight and other external egg quality traits, such as egg length (r = 0.71, 0.74, 0.64, and 0.78), egg width (r = 0.79, 0.81, 0.83, and 0.87), and egg surface area (r = 0.95, 0.89, 0.92, and 0.97) in pearl grey, lavender, royal purple and white varieties of domesticated helmeted guinea fowl, respectively (Table 1). The correlation coefficients between egg weight and shell weight were both significant ($p \leq 0.05$) and moderate (r = 0.42, 0.58, 0.35, and 0.69) in pearl grey, lavender, royal purple, and white varieties of domesticated helmeted guinea fowl, respectively. Moreover, significant positive correlations between egg weight, egg length, and egg width in different

varieties of guinea fowl were consistent with the obtained results of the studies conducted by Alkan et al. (2013) and Madibela et al. (2012). Regarding helmeted guinea fowl, egg weight, egg length, and egg width had higher correlation coefficients in this study were higher, compared to the obtained results of the same traits reported by Madibela et al. (2012). The white variety had the highest correlation coefficient of egg weight with length, width, surface area, and shell weight of the four varieties of helmeted guinea fowl. Therefore, the selection for increased egg weight (current egg grading system based on egg weight) can lead to the greatest improvements in egg length, width, surface area, and shell weight in the white variety, compared to the other three varieties.

Table 1. Phenotypic correlations among egg quality traits in pearl grey, lavender, royal purple, and white varieties of domesticated helmeted guinea fowl

Varieties	TRAIT	EW	EL	EWD	ESI	AWT	YWT	EC	SWT	STH	ESA	EV
PG	EW	1.000	0.713*	0.790*	-0.169	0.092	0.125	0.130	0.419*	-0.057	0.951*	0.967*
L		1.000	0.744*	0.805*	-0.257*	0.040	0.344*	0.203	0.584*	0.045	0.892*	0.908*
RP		1.000	0.640*	0.830*	-0.099	0.018	-0.132	-0.060	0.345*	0.020	0.919*	0.968*
W		1.00	0.776*	0.870*	-0.086	-0.156	-0.194	-0.176	0.685*	0.275	0.972*	0.979*
PG	EL		1.000	0.203*	-0.796*	0.013	0.078	0.047	0.191	-0.149	0.852*	0.685*
L			1.000	0.487*	-0.779*	-0.080	0.206	0.046	0.446*	0.020	0.913*	0.818*
RP			1.000	0.173	-0.820*	0.055	-0.136	-0.035	0.376*	-0.056	0.864*	0.699*
W			1.00	0.467*	-0.680*	-0.161*	-0.209	-0.184	0.744*	0.299	0.867*	0.740*
PG	EWD			1.000	0.430*	0.104	0.129	0.141	0.262*	-0.026	0.685*	0.852*
L				1.000	0.186	0.175	0.357*	0.306*	0.442*	0.088	0.787*	0.890*
RP				1.000	0.414*	0.063	0.067	0.083	0.124	0.004	0.645*	0.824*
W				1.00	0.383*	-0.061	-0.141	-0.086	0.439*	0.198	0.813*	0.917*
PG	ESI				1.000	0.052	-0.001	0.039	-0.018	0.122	-0.363*	-0.106
L					1.000	0.215	0.037	0.174	-0.185	0.043	-0.458*	-0.280
RP					1.000	-0.025	0.111	0.043	-0.274*	0.063	-0.425*	-0.171
W					1.00	0.114	0.102	0.118	-0.408*	-0.159	-0.225	-0.013
PG	AWT					1.000	0.256*	0.890*	0.137	0.039	0.064	0.081
L						1.000	0.306*	0.877*	0.012	0.048	0.028	0.074
RP						1.000	0.211	0.841*	0.030	0.102	0.079	0.086
W						1.00	0.704*	0.986*	-0.121	-0.339	-0.152	-0.135
PG	YWT						1.000	0.669*	0.114	-.0.169	0.127	0.135
L							1.000	0.726*	0.249	-0.055	0.311*	0.338*
RP							1.000	0.707*	0.035	0.106	-0.089	-0.049
W							1.000	0.827*	-0.100	-0.141	-0.224	-0.208
PG	EC							1.000	0.159	-0.500	0.109	0.126
L								1.000	0.134	0.006	0.177	0.224
RP								1.000	0.041	0.132	0.007	0.035
W								1.000	-0.122	-0.306	-0.180	-0.163
PG	SWT								1.000	0.384*	0.280*	0.292*
L									1.000	0.133	0.517*	0.519*
RP									1.000	0.503*	0.359*	0.313*
W									1.000	0.522*	0.715*	0.646*
PG	ESA										1.000	0.965*
L											1.000	0.981*
RP											1.000	0.964*
W											1.000	0.977*

*: $P \leq 0.05$; PG: Pearl grey; L: Lavender; RP: Royal purple; W: White varieties; EW: Egg weight; EL: Egg length; EWD: Egg width; ESI: Egg shell index; AWT: Albumin weight; YWT: Yolk weight; EC: Egg content; SWT: Shell weight; STH: Shell thickness; ESA: Egg surface area; EV: Egg volume.

Negative correlations were recorded between egg weight and egg shape index in all the four varieties of helmeted guinea fowl and between egg weight and shell thickness in the pearl grey variety. Islam and Dutta (2010) also reported negative correlations between egg weight and shape index (r= -0.17, -0.21, -0.21, -0.49, 0.05) in indigenous, exotic, and crossbred chickens of Rajshahi, Bangladesh. A negative association between egg weight and egg shape index has also been reported in other poultry species (Dzungwe et al., 2018; Godson et al., 2020). Duman et al. (2016) however reported a significant positive association between egg shape index and egg weight implying that heavier eggs are rounder in shape than lighter eggs. A negative association between egg weight and eggshell thickness suggests that heavier eggs are more thin-shelled and therefore more prone to breakages than lighter eggs. Strong, significant, and positive correlation coefficients between egg weight and other egg quality parameters indicated that selection for higher egg weight in guinea fowls might lead to simultaneous positive improvements in egg length, egg width, and egg surface area. However, it might negatively affect eggshell thickness which would lead to large eggs that are more prone to breakages.

Egg length had a significant positive association with egg surface area (r = 0.85, 0.91, 0.86, 0.87), egg volume (r = 0.69, 0.82, 0.70, 0.74), and weak positive association with egg width (r = 0.20, 0.49, 0.17, 0.47) in the pearl grey, lavender, royal purple and white varieties of domesticated helmeted guinea fowl, respectively. Weak correlation coefficients between egg length and egg width in all the four varieties of domesticated helmeted guinea fowl found in the current study were consistent with a study performed by Madibela et al. (2012) who reported a weak positive correlation between egg length and width (r = 0.25) in guinea fowls. Yakubu et al. (2008) found a strong and positive association correlation between egg length and width (r=0.71) in Nigerian indigenous chickens. Alkan et al. (2013) also contented moderate and positive correlation coefficients between egg length and width in pearl grey and royal purple varieties of helmeted guinea fowl. Egg surface area was also observed to have a high, significant ($p \leq 0.05$) and positive correlation coefficient with egg volume (r = 0.97, 0.98, 0.96, 0.98). Of the four varieties, the lavender variety had the highest correlation coefficient. Significant correlation coefficients between egg length, width, and surface were due to the fact that egg length and width can determine the volume and holding capacity of an egg, which in turn gives an indication of egg surface area and egg weight (Alkan et al., 2013). This implies that direct selection for either egg length or width will result in simultaneous improvement in egg volume, surface area, and weight. A weak, positive, and non-significant correlation coefficient was observed between egg length and eggshell weight in the pearl grey variety (r=0.19) while other varieties had moderate and significantly positive correlation coefficients. Negative and non-significant correlation coefficients were observed between egg length and eggshell thickness in pearl grey and royal purple varieties (r=-0.15 and -0.06, respectively) while other varieties were of weak, positive, and non-significant correlation coefficients. Strong, positive, and significant correlation coefficients existed among egg width, surface area, and volume in all four varieties indicating that egg surface area and volume increase with the growth of egg width. Consequently, the direct selection for egg width will result in simultaneous improvement in egg surface area and volume. There was a weak to moderate and significant correlation coefficient between egg width and shell weight in all the varieties of helmeted guinea fowl except for the royal purple which had a weak non-significant correlation coefficient. Weak to moderate correlation coefficients between egg width and shell weight observed in the four varieties of guinea fowl were consistent with Yakubu et al. (2008) who reported a weak association between egg width and shell weight (r=0.19) in Nigerian indigenous chicken. A moderate, positive and significant correlation between egg width and egg shape index occurred in the pearl grey, royal purple, and white varieties (r=0.43, 0.41, and 0.38, respectively) while a weak, positive and non-significant correlation coefficient was observed between the two traits in the lavender variety. Negative, moderate, and significant correlations occurred between egg shape index and surface area in the different varieties of domesticated helmeted guinea fowl except for the white variety which showed a negative but non-significant correlation coefficient (r= -0.23). Ultimately, weak, positive and non-significant correlation coefficients were also observed between egg shape index and shell thickness in the different varieties of domesticated helmeted guinea fowl except white variety which indicated a negative but non-significant correlation coefficient (r=-0.16).

Phenotypic correlations among internal egg quality traits

Strong, positive, and significant correlations occurred between albumin weight and egg content (r = 0.89, 0.88, 0.84, and 0.99), and weak non-significant correlations were observed between albumin weight and

egg volume (r = 0.08, 0.07, 0.07, and -0.14) in the pearl grey, lavender, royal purple and white varieties of guinea fowl, respectively. Weak, positive, and significant correlations occurred between albumin weight and yolk weight (r = 0.26 and 0.31) in pearl grey and lavender variety**,** respectively. The correlation coefficients between albumin weight and yolk weight in pearl grey and lavender were consistent with Udoh et al. (2012) who also recorded a weak, positive, and significant correlation between albumin weight and yolk weight in naked neck local chickens (r = 0.28). Yolk weight was strongly, positively, and significantly correlated with egg content (r = 0.67, 0.73, 0.71, and 0.83) in the pearl grey, lavender, royal purple, and white varieties. However, negative, non-significant correlation coefficients were observed between yolk weight and egg volume in the pearl grey and white varieties (r = -0.14 and -0.05, respectively). In addition, a weak, positive, and significant correlation coefficient was observed between the two traits in the lavender variety. The most desirable egg should preferably have more albumin weight (more protein) and less yolk weight (less fat).

Phenotypic correlations between external and internal egg quality traits

There was a strong, positive, and significant correlation between egg weight and volume (r = 0.97, 0.91, 0.97 and 0.98), while egg weight showed weak, non-significant, both negative and positive correlations with other internal quality traits, such as albumin weight (r = 0.09, 0.04, 0.02 and -0.16), yolk weight (r = 0.13, 0.34, -0.13 and -0.19), and egg content (r = 0.13, 0.20,-0.06 and -0.18) in pearl grey, lavender, royal purple, and white varieties of guinea fowl, respectively. A strong correlation coefficient between egg weight and volume was observed in all the four varieties of guinea fowl that were consistent with the reported findings of Islam and Dutta (2010) who mentioned a strong positive correlation coefficient between egg weight and volume (r = 0.93) in the Sonali chicken breed of Bangladesh. The white variety had the highest correlation coefficient between egg weight and volume, while the pearl grey had the highest correlation coefficient between egg weight and albumin weight.

Strong, positive, and significant ($p \leq 0.05$) correlations existed between egg length and volume (r = 0.69, 0.82, 0.70, and 0.74) in the pearl grey, lavender, royal purple, and white varieties of guinea fowl, respectively. Weak and positive correlations (r = 0.05 and 0.05) were observed between egg length and content in pearl grey and lavender varieties, respectively, and negative correlations (-0.04 and -0.18) were observed between egg length and egg content in royal purple and white varieties, respectively. All the correlation coefficients between egg length and egg content were non-significant in all the four varieties of helmeted guinea fowl. Weak, non-significant, positive correlations existed between egg width and albumin weight (r = 0.10, 0.18, 0.06 and -0.06), egg content (r = 0.14, 0.31, 0.08 and -0.09) and egg yolk weight (r = 0.13, 0.36, 0.07 and -0.14) while strong, positive and significant correlations were observed between egg width and egg volume (r = 0.85, 0.89, 0.82 and 0.92) in the pearl grey, lavender, royal purple and white varieties of helmeted guinea fowl, respectively. Weak, positive correlation coefficients between egg width and albumin weight observed in all the four varieties of guinea fowl were not in the same line with the obtained results of a study conducted by Yakubu et al. (2008) indicating a moderate, positive, and significant correlation coefficient between egg width and albumin weight (r = 0.57) in the free-range naked neck and full feathered chickens. Weak, non-significant positive correlation coefficients existed between egg surface area and albumin weight (r= 0.06, 0.03, 0.08, and -0.15), egg content (r=0.11, 0.18, 0.007, and -0.18) and yolk weight (r= 0.13, 0.31, -0.09, and -0.22) while strong, positive and significant correlations existed between egg surface area and volume (r = 0.97, 0.98, 0.96, and 0.98) in the pearl grey, lavender, royal purple and white varieties of helmeted of guinea fowl, respectively.

Egg volume was weakly and positively correlated with albumin weight (r = 0.08, 0.07, 0.07 and -0.14), egg content (0.13, 0.22, 0.04 and -0.16), and yolk weight (0.14, 0.34, -0.05 and -0.21) in the pearl grey, lavender, royal purple and white varieties of guinea fowl, respectively. Weak, negative, and non-significant correlations existed between egg shape index and egg volume (r = -0.11, -0.28, -0.17, and -0.01) while weak, positive, and non-significant correlations existed between egg shape index and egg content (0.04, 0.17, 0.04, and 0.12) in the pearl grey, lavender, royal purple and white varieties of helmeted guinea fowl, respectively. Egg shape index was weakly, positive to negative, and non-significantly correlated with albumin weight (r = 0.05, 0.22, -0.03 and 0.11) and yolk weight (r = - 0.001, 0.04, 0.11, and 0.10) in the pearl grey, lavender, royal purple and white varieties of domesticated helmeted guinea fowl, respectively. Weak, positive, and non-significant correlation coefficients between egg shape index and albumin weight were consistent with Islam and Dutta (2010) who also reported weak, positive, and non-

significant correlation coefficients between the two traits in five genetic groups of chicken in Rajshahi (r = 0.27, 0.10, -0.15, -0.44 and -0.13), respectively.

Weak, positive, and non-significant correlations existed between shell weight and albumin weight, yolk weight, and egg content in all the four varieties of helmeted guinea fowl. Weak and moderate, positive, and significant correlations were observed between shell weight and egg volume (r = 0.29, 0.52, 0.31, and 0.65) in the pearl grey, lavender, royal purple, and white guinea fowl varieties, respectively. Shell thickness was weakly and non-significantly correlated with egg content and yolk weight in all the varieties of helmeted guinea fowl.

The lavender variety had the highest correlation coefficient between various internal and external egg quality characteristics. It had the highest correlation coefficients with egg width and albumin weight, egg content, and yolk weight. The lavender variety also exhibited higher correlation coefficients between egg surface area and egg volume, egg content, and yolk weight as well as between egg volume and egg content and yolk weight. Improvements in external egg quality characteristics (egg weight, egg length, egg width) in guinea fowl are, therefore, likely to also lead to the greatest improvements in internal egg quality traits in lavender than other guinea fowl varieties.

CONCLUSION

Selection for higher egg weight in guinea fowl may lead to simultaneous improvements in egg length, width, shell weight, surface area, and volume. It might, however, negatively affect the egg shape index and shell thickness in all the four varieties of domesticated helmeted guinea fowl. Among the four varieties of helmeted guinea fowl, the white variety had the strongest correlation coefficients with various external egg quality traits and various internal egg quality characteristics. The lavender variety had the highest correlation coefficients with internal and external egg quality characteristics. The white and lavender guinea fowl varieties will therefore be more responsive than the pearl and royal purple varieties for selection of egg-type or layer type guinea fowl.

DECLARATIONS

Acknowledgements

The authors would like to thank the Botswana University of Agriculture and Natural Resources for funding the study.

Competing interests

The authors declare that they have no competing interest

Author's contributions

P Kgwatalala designed the research. F Manyeula and O Tumagole performed the research and wrote the manuscript. All authors read and approved the final version of the manuscript.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 587-598, December 25, 2020

Research Paper, PII: S2322455X2000067-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.67

Polymorphism of the Prolactin Gene in Egyptian Duck Breeds

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Received: 18 Oct. 2020
Accepted: 07 Dec. 2020

ABSTRACT

In avian, the prolactin hormone triggers and regulates ovarian follicle development. This study aims to detect the Prolactin (*PRL*) gene polymorphisms (exons 1and5) in four Egyptian duck breeds, namely Campbell, Moulard, Muscovy, and Pekin using PCR-RFLP technique and sequence analysis. It also investigated the association of this gene with egg production, egg weight, and body weight. The present results revealed that *PRL* gene exon 1 and part of intron 1 showed two alleles A and B (polymorphic) in each of Campbell and Moulard, however, Muscovy and Pekin had only one allele (monomorphic). The allele A was more dominant with frequencies of 0.70, 0.60, and 1.00, compared to the allele B (0.30, 0.40, and 0.00) for Campbell, Moulard, and Muscovy, respectively. For Pekin, the allele B only appeared with the frequency of 1.0. Ducks with the high frequency of allele A were superior at egg weight, compared to others. Furthermore, for *PRL* gene exon 5, there were two alleles G and C (polymorphic) in Campbell, Moulard, and Muscovy, however, Pekin had only one allele (monomorphic). The allele G was more dominant (0.15, 0.74, 0.0, and 0.84) than the allele C (0.85, 0.26, 1.0, and 0.15) for Campbell, Moulard, Pekin, and Muscovy, respectively. Ducks having a high frequency of allele C were superior at egg production. Furthermore, there were many single nucleotide polymorphisms (SNPs) in the sequences in all breeds. The utmost ones exist at the restriction sites of *Xba*I enzyme for the amplified fragment, in the promotor, exon 1 and intron 1 (T378C in intron 1), and *Dra*I enzyme for that in exon 5 (A5871G in exon 5).

Keywords: Duck, Genetic polymorphism, Genotyping, Prolactin gene

INTRODUCTION

Meat and eggs of ducks have a high nutritional value for humans. Ducks are foremost raised in small rural farms to produce eggs and meat to improve economic livelihood. Ducks have great economic importance to many countries (Narhari, 2009). The Pekin duck (*Anas platyrhynchos domestica*), Muscovy duck (*Cairina moschata*), and Moulard ducks (crossing between Muscovy and Pekin duck), are the main duck species that are used globally to produce meat of ducks (Baeza, 2006). The Muscovy duck (*Cairina moschata*) meat has a distinct taste, with low calories, so it has global economic importance (Veeramani et al., 2016). The Muscovy and Moulard are characterized by lower fatness and higher meat production as compared by Pekin ducks (Wawro et al., 2004). The Campbell duck (*Anas platyrhynchos*) is a high egg-production breed. Moreover, the nutritional value of duck eggs is higher than chicken ones, in its mineral salts, vitamins, and amino acids (Sadar et al., 2014).

Traditional breeding approaches of selection and crossbreeding have improved the productivity of duck and devised new hybrids, while improvement using this method was slow (Asiamah et al., 2019). Duck productivity was increased using modern methods of molecular genetics, by identifying candidate genes associated with quantitative traits to improve productive traits and enhance breeding programs (Basumatary et al., 2019). One of the utmost serious problems in farming ducks is the low productivity and quality of production. Therefore, their genetic improvement aims to increase productivity, improve product quality and elevate economic value (Chang et al., 2012). Genetic improvement programs using traditional and modern methods for meat-type ducks have successfully enhanced their productive performance. In Pekin ducks, the genetically improved type for higher meat production reached to 3.2 kg at seven weeks, while unimproved duck production reached to 1.7 kg at 11 weeks of age (Zeng et al., 2016).

To cite this paper: Sabry NM, Mabrouk DM, Abdelhafez MA, El-Komy EM and Mahrous KF (2020). Polymorphism of the Prolactin Gene in Egyptian Duck Breeds. *J. World Poult. Res.*, 10 (4): 587-598. DOI: https://dx.doi.org/10.36380/jwpr.2020.67

Prolactin hormone gene (*PRL*) is a single-chain polypeptide belongs to the family of growth hormone genes, and synthesized by the anterior pituitary gland of poultry (Wang et al., 2011). The size of duck prolactin gene is 1000 bp in size and consists of five exons and four introns encoding 229 amino acids. As the chicken *PRL* gene was cloned and sequenced (Watahiki et al., 1989), a bulk of studies have targeting this gene polymorphism (Xu et al., 2015; Shamsalddini et al., 2016; Li et al., 2017). In recent years, polymorphisms in the *PRL* gene have been associated with egg production in hens (Sarvestani et al., 2013; Kulibaba, 2015; Tempfli et al., 2015; Mohamed et al., 2017; Yadav et al., 2018; Bai et al., 2019; Basumatary et al., 2019).

Identifying single nucleotide polymorphisms (SNPs) in candidate genes and their association with egg laying traits is an important technique used to enhance the avian genetics (Feng et al., 2018). Therefore, the present study used four Egyptian duck breeds; Moulard, Campbell, Pekin and Muscovy ducks to screen polymorphism of the duck *PRL* gene. Identifying of such SNPs can be employed as genetic markers for selection of genetically superior ducks to increase productivity.

MATERIALSANDMETHODS

Ethical approval

Permission for collecting the samples used in this work was received from the management of El-Nubaria farm, owned by National Research Centre that was included in this study. The samples were collected per standard sample collection procedures without any harm to animals.

Animals

The present study used a total of 60 healthy ducks, of four breeds; Campbell, Moulard, Muscovy and Pekin, raised in El-Nubaria experimental farm, owned by the National Research Centre-Giza-Egypt. 15 blood samples (3mL) were aseptically collected from each breed, using EDTA (0.5 M) as an anticoagulant.

DNA Extraction

Genomic DNA was isolated from whole blood of ducks using salting out method (Shokrzadeh and Mohammadpour, 2018), with minor modifications. Briefly, blood (3 ml) was mixed with cell lysis buffer (640 mM sucrose, 10 mM $MgCl_2$, 20 mM Tris-HCl, 2% Triton 100X) and placed on ice for 30 min then centrifuged at 5000 rpm for 15 min at 4°C and the supernatant was discarded. Nuclei lysis buffer (10 mM Tris-base, 400 mM NaCl, 2 mM EDTA) was added to the pellet and mixed with 20% Sodium Dodecyl Sulfate (SDS) and proteinase K then placed in a water bath at 55°C for two hours. NaCl (saturated) was added and centrifuged to separate a clear upper layer containing DNA. Only 30 µl of the clear layer was transferred to a tube containing absolute ethanol to fish the DNA and dissolved in TE buffer (10 mM Tris-HCl, 1 mM EDTA) at 37°C for 2 hours. Purity and concentration of DNA were measured using Nano Drop™ 1000 Spectrophotometer (Thermo Fisher Scientific, USA). Extracted DNA was stored in -20°C till usage.

Polymerase Chain Reaction (PCR)

The primers used were F: 5'-AAATTCCCTCTCACAG TTACA-3'; R: 5'-GATGCAGAGACAAGTTTCACC-3' for PRL (intron 1) to produce a product of 417 bp and F: 5'-TGCAAACCATAAAAGAAAAGA-3'; R: 5'-CAATGAAAAGTGGCAAAGCAA-3' for *PRL* (exon 5) to produce a product of 400 bp. PCR amplification was carried out in a 25 µl reaction volume, including 2 µl genomic DNA (50 ng), 2.5 µL 10X buffer, 2.5 mM of deoxyribonucleotide triphosphates (dNTPs), 2.5 µl of each primer (10 pmol), and 0.5 µl *Taq* polymerase (Thermo-Fisher Scientific, USA). The PCR conditions were; 5 min at 94°C, followed by 35 cycles of 1 min at 94°C, 30 sec at the annealing temperature 54°C, 2 min at 72°C and a final extension of 7 min at 72°C.

Restriction Fragment Length Polymorphism (RFLP)

Digestion of the PCR products was performed overnight at 37°C in a final volume of 30 µl with specific restriction enzymes (Thermo Fisher Scientific, USA); *Xba* I (5'T↓CTAGA-3') for PRL (Intron 1), and *DraI* (5 'TTTAAA↓3') for PRL (Exon 5). The RFLP reaction mixture composed of 10 µL of PCR products, 1U of restriction enzymes, 2 µl of buffer and 18 sterile H_2O. The digested products were run in 2.5% agarose gel and different genotypes were visualized under U.V. transilluminator and photographed using Gel documentation system.

DNA Sequencing and Analysis

The PCR products were purified using Gene JET Gel Extraction Kit (Thermo-Fisher Scientific, USA) according to the manufacture instructions. The purified PCR products were sequenced using an automated sequencing service (Macrogen, South Korea). Sequence analysis was

performed via program BLAST/NCBI (National Center for Biotechnology Information. http://www.ncbi.nlm.nih.gov/). Sequence alignment were accomplished by Clustal Omega version (1.2.4) (https://www.ebi.ac.uk/Tools/msa/clustalo), as described by (Larkin et al., 2007). The phylogenetic trees between the studied breeds, and other avian were done, using unweighted pair group method with arithmetic mean (UPGMA). To detect chromosomal localization of prolactin gene (exons 1 and 5) from Egyptian duck breeds in the duck genome, *Anas platyrhynchos* isolate PK-2015, IASCAAS_PekingDuck_PBH1.5, was used from NCBI.

RESULTS

In the current study, the DNA fragment (417 bp), covering the *PRL* gene promoter (220 bp), exon 1 (28 bp) and part of intron 1 (169 bp), was successfully PCR amplified, as well as the other fragment (400 bp), covers the coding region of *PRL* gene exon 5 (192 bp), and part of intron 4 (137 bp, Figure 1a).

The *Xba*I/RFLP for *PRL* (the promoter, exon 1 and part of intron 1) revealed three fragments; non-cut fragment (417 bp) or homozygous genotype (AA), cut fragments (356 bp and 61 bp) or homozygotes (BB) [61 bp band is not visible because it is too short], and the combined fragments (417 bp, 356 bp and 61 bp) or heterozygotes (AB Figure 1b). As illustrated in Table 1, both Campbell and Moulard breeds are polymorphic resulted two alleles (A and B). However, Muscovy (A) and Pekin (B) were monomorphic resulted one allele. The allele A frequency was much higher than allele B in the four breeds. The results revealed that the four investigated duck breeds, PRL gene exon 1 and part of intron 1, had two alleles (A and B) and three genotypes AA, AB, BB, ducks with higher frequency of allele A superior at egg weight, at 10-weeks-old body weight compared to other duck breeds (Table 1).

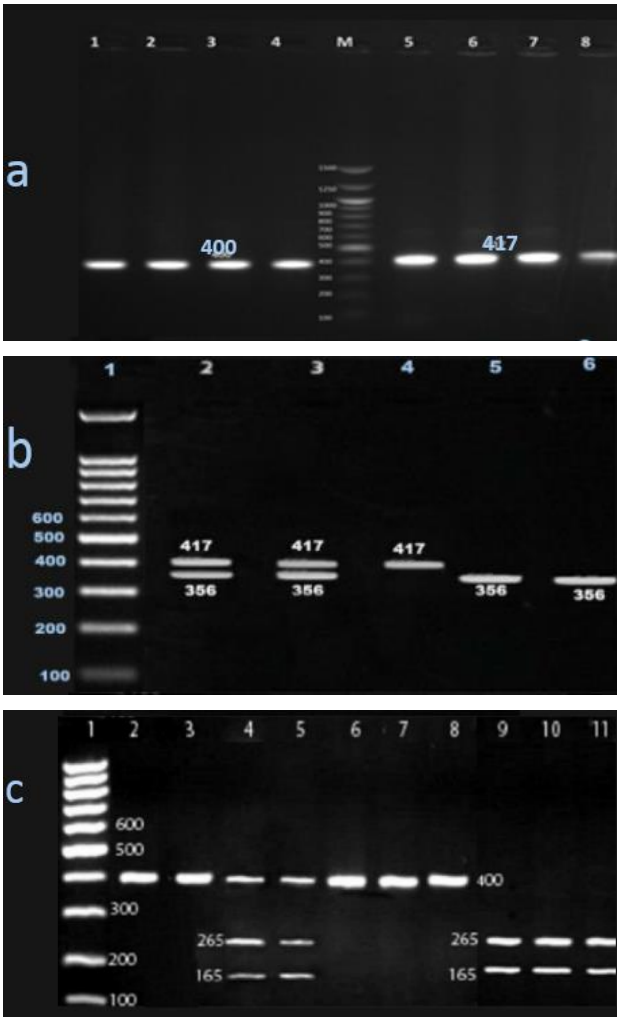

Figure 1a. Electrophoresis of the PCR products of prolactin exons 1 and 5 on agarose gel. Gel was stained with ethidium bromide, Lane 1-4: prolactin (exon5), Lanes 5-8: prolactin (exon1), Lane M: 100-bp DNA ladder. **Figure 1b.** Electrophoresis of the digestion products of *Xba*I on agarose gel. Gel was stained with ethidium bromide, Lanes 2 and 3: AB genotype, Lane 4: AA genotype, Lanes 5 and 6: BB genotype, Lane 1: 100-bp ladder. **Figure 1c.** Electrophoresis of the digestion products of *DraI* on agarose gel. Gel was stained with ethidium bromide, Lane 2, 6, 7, and 8: AA genotype, Lanes 4 and 5: AB genotype, Lanes 9, 10 and 11: BB genotype, Lane 1: 100-bp DNA Ladder.

Table 1. Relation between the four Egyptian duck breeds (Campbell, Moulard, Pekin and Muscovy) and body weight, egg number per year and egg weight, allelic and genotypic frequencies

Breed	BW10	Eggs number /year	Egg weight	Allelic Frequency				Genotypic Frequency					
				Exon 1		Exon 5		Exon 1			Exon 5		
				A	B	G	C	AA	AB	BB	GG	CG	CC
Campbell	1306.57±37.32	300-320	65 g	00.70	00.30	0.15	0.85	0.50	0.40	0.10	0.15	0.00	0.85
Moulard	4021.00±20.49	200-230	60 g	00.60	00.40	00.74	00.26	0.35	0.50	0.15	0.61	0.26	0.13
Pekin	2846.00±30.02	200-300	60 g	00.00	1.00	0.00	1.00	0.00	0.00	1.00	0.00	0.00	1.00
Muscovy	3740.00±47.37	100-180	77 g	1.00	00.00	00.85	00.15	1.00	0.00	0.00	0.75	0.20	0.05

In similar manner, *Dra*I/RFLP for *PRL* (exon 5) yielded two homozygous genotypes were GG (400 bp), CC (235 and 165 bp) and heterozygotes are known as genotypes GC (400, 235 and 165 bp, Figure 1c). As illustrated in Table 1, all races are polymorphic, except Pekin which was monomorphic (C). Besides, the allele G was more dominant than allele C in the four races. Additionally, *PRL* gene exon 5 of the four manipulated duck breeds, at 10-weeks-body-old weight, had two alleles (G and C) and three genotypes GG, GC, CC, ducks that had high frequency of allele C were superior at egg production compared with the other ducks (Table 1).

Genetic polymorphisms of *PRL* gene covers the coding region of *PRL* gene (promoter, exon 1 and part of intron 1 and exon 5) between the four Egyptian duck breeds also can be detected by DNA-sequencing methods, Clustal Omega was used to aligned each breed of the four Egyptian duck breeds with each other and with *Anas platyrhynchos*, *PRL* gene, cds, AB158611 (*A. platyrhynchos*, *PRL*) presented in the database. The Moulard breed samples revealed that Moulard-1 sequences shared similarity (97.36%) with Moulard-2. Also, the DNA sequence from Campbell breed samples revealed that the Campbell-1 sequence shared similarity (97.36%) with Campbell-2. However, Moulard-1 sequences shared high similarity (100%) with Campbell-2, and Moulard-2 sequences shared high similarity (100%) with Campbell-1. The alignment between Moulard-1 and Campbell-2 with both Moulard-2 and Campbell-1 showed that Four nucleotide substitutions at nucleotide 132 (A/G), 166 (T/C), 213 (C/T) and 378 (T/C), this mutation are considered from the transition type, the other seven nucleotide substitutions at nucleotide 319, 325, 332 (T/G), 318, 322, 326, 330 (G/T) the SNPs between the sequences are considered from the transversion type.

Furthermore, *A. platyrhynchos*, *PRL* shared similarity (99.04%) with Moulard-1 and Campbell-2 sample, two nucleotide substitutions at nucleotide 267 (G/A) and at nucleotide 412 (A/G), these mutations are considered from the transition type, the other two nucleotide substitutions at nucleotides 312 (T/G) and 314 (G/T), are considered from the transversion type. Both Moulard-2 and Campbell-1 samples shared similarity (96.40%) with *A. platyrhynchos*, *PRL*, six nucleotide substitutions at nucleotide 132 (A/G), 166 (T/C), 213 (C/T), 267 (G/A), 378 (T/C) and 412 (A/G), the mutations are considered from the transition type, the other nine nucleotide substitutions at nucleotides 312, 319, 325, 332 (T/G), 314, 318, 322, 326, 330 (G/T), are considered from the transversion type (Figure 2) and percent identity matrix of the multiple sequence alignment (Table 2).

The genomic sequences of *PRL* gene from Pekin and Muscovy breeds revealed that the sequences (Pekin-1 and Pekin-2) also, (Muscovy-1 and Muscovy-2) shared high similarity (100%) between each other as there is no SNPs between the sequences. However, all Pekin breed samples shared similarity (98.32%) with *A. platyrhynchos*, *PRL* (Table 2). Eight transitions at nucleotides; 267 (G/A) and 412 (A/G). In addition, five transversions at nucleotides; 135 (T/A), 137(C/G), 213(C/T), 312 (T/G) and 314 (G/T). All Muscovy ducks shared similarity (96.40%) with *A. platyrhynchos*. Six transitions at nucleotides; 132 (A/G), 166 (T/C), 213 (C/T), 267 (G/A), 378 (T/C), 412 (A/G), and nine transversions at 312, 319, 325, 332 (T/G), 314, 318, 322, 326, 330 (G/T), were found (Figure 2).

Sequence comparisons among the four studied breeds *PRL* gene exon1 sequence revealed that Moulard-1 revealed high similarity (100%) with Campbell-2, (99.28%) with Pekin and (97.36%) with Moulard-2, Campbell-1 and Muscovy. As Muscovy resulted high similarity (100%) with Campbell-1 and Moulard-2, (97.12%) with Pekin (Table 2).

The four examined duck lines, *PRL* gene exon 5 sequence, aligned with *A. platyrhynchos*, *PRL* disclosed upraised similarity (100%) with all Pekin (Pekin-1 and Pekin-2), Moulard-2, Campbell-2 and also Muscovy-1. However, *A. platyrhynchos*, *PRL* illustrated similarity (97.25%) with Moulard-1, Campbell-1 and Muscovy-2 (Table 3). There were five transitions at nucleotides; 5780 (G/A), 5808(T/C), 5822(C/T), 5871(A/G), 5926(G/A), and six transversions at nucleotides; 5766 (G/T), 5792 (A/T), 5834 (G/T), 6004 (A/C), 6007(G/C) and 6029(G/T) (Figure 3). For the sequence comparisons among the four checked duck breeds exon 5 revealed that Moulard-1 exhibited high similarity (100%) with Campbell-1, Muscovy-2, but 97.25% with Moulard-2, Campbell-2, Muscovy-1, Pekin-1 and Pekin-2 (Table 3).

The obtained sequences were submitted to Gen bank and have been assigned with accession number; Campbell *PRL* exon1 allele A (LC565022) and allele B (LC565023), Moulard *PRL* exon 1 allele A (LC576823) and allele B (LC565024), Pekin *PRL* exon 1 (LC565026), Muscovy *PRL* exon 1 (LC565025). Also, the obtained sequences for exon 5 were submitted, Campell *PRL* exon 5 allele A (LC565015) and allele B (LC565016), Moulard *PRL* exon 5 allele A (LC565017) and allele B (LC565018), Pekin *PRL* exon 5 (LC565021), Muscovy PRL exon 5 allele A (LC565019) and allele B (LC565020).

Table 2. Percent Identity Matrix of DNA multiple sequence alignment for the four Egyptian duck breeds (Campbell, Moulard, Pekin and Muscovy) with each other and other avian species sequences of *PRL* gene exon 1 published in GenBank database

Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1: *M. gallopavo*	100.00	77.27	78.64	76.50	76.50	76.50	76.92	76.50	76.50	76.50	85.88	84.71	97.37	94.12
2: *C. moschata*		100.00	91.86	98.72	98.72	98.72	97.28	97.45	97.45	97.02	90.10	86.96	87.55	86.25
3: *A. anser*			100.00	94.19	94.19	94.19	93.84	95.64	95.64	95.40	90.50	87.90	85.89	82.89
4: Campbell-1,allele A				100.00	100.00	100.00	96.40	97.36	97.36	97.12	89.30	86.75	88.44	84.73
5: Moulard-2 allele A					100.00	100.00	96.40	97.36	97.36	97.12	89.30	86.75	88.44	84.73
6: Muscovy-1,2						100.00	96.40	97.36	97.36	97.12	89.30	86.75	88.44	84.73
7: *A. platyrhynchos*							100.00	99.04	99.04	98.32	88.48	85.94	87.85	84.18
8: Campbell-2 allele B								100.00	100.00	99.28	88.89	86.35	88.00	84.36
9: Moulard-1 allele B									100.00	99.28	88.89	86.35	88.00	84.36
10: Pekin-1,2										100.00	88.48	85.94	87.56	84.00
11: *C. japonica*											100.00	97.11	96.41	91.67
12: *P. cristatus*												100.00	95.57	92.34
13: *G. gallus* B allele													100.00	94.20
14: *P. colchicus*														100.00

1: *Meleagris gallopavo PRL* AB605394, 2: *Cairina moschata PRL*, KM390982, 3: *Anser anser PRL*, GU984377, 4: Campbell-1 *PRL* Ex-1, LC565022, 5: Moulard-2 allele A, LC576823, 6: Muscovy *PRL* Ex1, LC56502, 7: *A. platyrhynchos PRL*, AB158611, 8: Campbell-2 allele B, LC565023, 9: Moulard-1 allele B, LC565024, 10: Pekin, PRL Ex-1, LC565026, 11: *Coturnix japonica PRL*, AB452962, 12: *Pavo cristatus PRL*, AB452960, 13: *Gallus gallus PRL* B allele, JN661569, 14: *Phasianus colchicus PRL*, AB452961

Table 3. Percent Identity Matrix of DNA multiple sequence alignment for the four Egyptian duck breeds (Campbell, Moulard, Pekin and Muscovy) with each other and other avian species sequences of *PRL* gene exon 5 published in GenBank database

Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1: *Struthio camelus*	100.0	87.17	87.17	87.17	87.96	87.96	87.96	87.96	87.96	88.74	81.98	81.34	81.68	83.76
2: Campbell-1 alleleA_Ex5		100.00	100.00	100.00	97.75	97.75	97.75	97.75	97.75	97.50	83.89	84.20	84.48	83.54
3: Moulard-1 allele A Ex5			100.00	100.00	97.75	97.75	97.75	97.75	97.75	97.50	83.89	84.20	84.48	83.54
4: Muscovy-2 allele B Ex5				100.00	97.75	97.75	97.75	97.75	97.75	97.50	83.89	84.20	84.48	83.54
5: *A. platyrhynchos*					100.00	100.00	100.00	100.00	100.00	98.75	85.68	86.65	85.75	85.09
6: Campbell-2 allele B Ex5						100.00	100.00	100.00	100.00	98.75	85.68	86.65	85.75	85.09
7: Moulard-2 allele B Ex5							100.00	100.00	100.00	98.75	85.68	86.65	85.75	85.09
8: Muscovy-1 allele A Ex5								100.00	100.00	98.75	85.68	86.65	85.75	85.09
9: Pekin-1,2									100.00	98.75	85.68	86.65	85.75	85.09
10: *A. anser*										100.00	85.93	86.38	86.51	86.34
11*: G. gallus*											100.00	94.57	93.61	93.50
12: *P. cristatus*												100.00	94.57	94.43
13*: M. gallopavo*													100.00	98.45
14: *Ph. Colchicus*														100.00

1: *Struthio camelus PRL* AB36288, 2: Campbell-1 *PRL* gene Ex5, LC56501, 3: Moulard-1 *PRL* gene Ex5, LC565017, 4: Muscovy-2 *PRL* gene Ex5, LC565020, 5: *A. platyrhynchos PRL*, AB158611, 6: Campbell-2 *PRL* gene Ex 5, LC565016, 7: Moulard-2 *PRL* gene Ex5, LC565018, 8: Muscovy-1 *PRL* gene Ex5, LC565019, 9: Pekin *PRL* gene Ex5, LC565021, 10: *Anser anser PRL*, GU984377, 11: *Gallus gallus PRL*, AB011438, 12: *Pavo cristatus PRL*, AB605393, 13: *Meleagris gallopavo PRL*, AH005340, 14: *Phasianus colchicus PRL*, AB605395

To cite this paper: Sabry NM, Mabrouk DM, Abdelhafez MA, El-Komy EM and Mahrous KF (2020). Polymorphism of the Prolactin Gene in Egyptian Duck Breeds. *J. World Poult. Res.,* 10 (4): 587-598. DOI: https://dx.doi.org/10.36380/jwpr.2020.67

Figure 2. Multiple DNA sequence alignment of *PRL* Ex1 of the four Egyptian duck breeds (Campbell, Moulard, Pekin and Muscovy) with the *Anas platyrhynchos PRL* gene Ex 1, AB158611, and nucleotide sequences of alleles A and B showing SNPs at nt 356 and the presence of *Xba*I restriction site (T↓CTAGA) in alleles B.

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Figure 3. Multiple DNA sequence alignment of *PRL* Ex5 of the four Egyptian duck breeds (Campbell, Moulard, Pekin and Muscovy) with the *Anas platyrhynchos PRL* gene Ex 5, AB158611, and nucleotide sequences of alleles G and C showing SNPs position at nt 165 and the presence of *Dra*I restriction site (3'AAA↓TTT 5') (underlined) in alleles C.

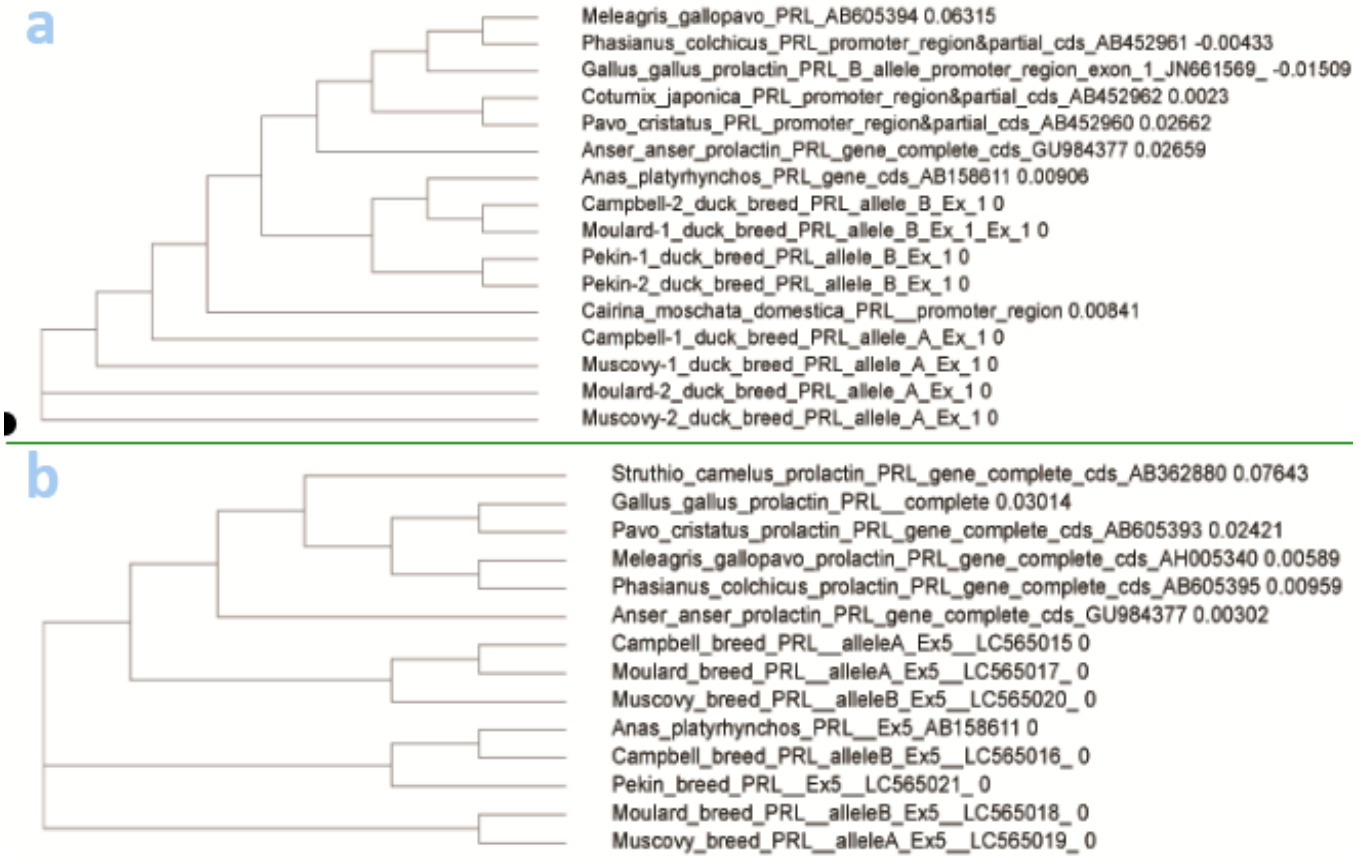

Figure 4a. Phylogenetic tree of the Multiple DNA sequence alignment of the four Egyptian duck breeds (Moulard, Pekin, Campbell and Muscovy) *PRL* gene exon 1 with the other sequences of avian prolactin gene species published in GenBank database. Figure 4b. Phylogenetic tree of the Multiple DNA sequence alignment of the Egyptian duck breed *PRL* gene exon 5 with the other sequences of avian prolactin gene species published in GenBank database.

Sequence comparison of *PRL* gene exon 1, between the four Egyptian duck breeds and other avian Species, appeared in percent identity matrix of DNA multiple sequence alignment of exon 1 (Table 2) and phylogenetic tree (Figure 4a). Likewise, DNA sequence comparison of exon 5, between the four breeds, and other birds, were illustrated in percent identity matrix of DNA multiple sequence alignment of exon 1 (Table 3) and phylogenetic tree (Figure 4b).

Regards to the phylogenetic tree, of Egyptian duck breeds, *PRL* gene exon1, the locus of Moulard-1 was related to Campbell-2 and Pekin, more than Moulard-2, Campbell-1 and Muscovy. However, the locus of Muscovy was related to Moulard-2, Campbell-1, more than Pekin (Figure 4a). For exon 5 tree, the locus of Moulard-1 was related to Campbell-2, Muscovy-2, more than Moulard-2, Campbell-2, Muscovy-1and Pekin (Figure 4b).

Lastly, prolactin gene sequence, in the four studied strains, was aligned with Duck genome, by using the BLAST program. The results of these alignments represent Duck prolactin (*PRL*) gene sequence on chromosome 2 (APL 2), *Anas platyrhynchos* isolate PK-2015 chromosome 2, IASCAAS Peking Duck PBH1.5 ranging from 49241262 to 49241678 for prolactin promoter exon 1 gene, and ranging from 49246949 to 49247348 for exon 5.

DISCUSSION

Research on the PRL gene have been widely carried out, the avian PRL gene is highly conserved and most

sequence polymorphisms in the PRL gene occur in 5′ flanking region, 3′ flanking region (Kansaku et al., 2008). The literatures focused on polymorphisms of PRL gene in 5′ flanking region (promoter region) which has been considered as an excellent experimental model for studying both tissue-specific and hormonally regulated activation of gene transcription The literature lightened up PRL gene polymorphism, in 5′ flanking region (promoter region) which has been respected as a perfect experiential example, for exploring both tissue-special and hormonally managed activation of gene transcription (Elsholtz et al., 1991; Li et al., 2009; Wang et al., 2011; Chang et al., 2012).

In this study, the results showed that Genetic polymorphisms of *PRL* gene by RFLP analysis, so the restriction enzymes *XbaI* and *DraI* have been used. The results of RFLP characterization analysis using the *Xba*I enzyme showed that the four Egyptian duck breeds PRL gene exon 1 and part of intron 1 at 10-weeks-old body weight had two alleles (A and B) and three genotypes AA, AB, BB, ducks with high frequency of allele A superior at egg weight compared to others. Into the bargain, the association of intron 1 polymorphism of *PRL* gene with egg weight was studied (Li et al., 2009) and agreed with present study. PCR-RFLP produced three genotypes AA, BB, and AB, and ducks of BB genotype were higher egg production and superior egg weight at 30 weeks than AB genotypes, which in agreement with this study. Wang et al. (2011) found variations in exons 2, 4 and 5 in local Chinese ducks, but the relationship with annual egg production was shown by exon 5. The prolactin gene SNP at intron 1, C→A mutation at position 386 at introns which can be detected by *Xba*I enzyme (Mazurowski et al., 2016), identifying two alleles G and T, and three genotypes GG, TG and TT. *PRL*/*XbaI* locus was found polymorphic in Pekin and Moulard duck populations, while monomorphic in Muscovy duck breed. Thus, the result would be useful as a control for genetic equilibrium in Muscovy ducks. In addition, Bai et al. (2019) studied the association between *PRL* gene with egg production. They found three genotypes AA, AG, GG and ducks that have GG genotype were greater in egg weight and egg production when compared to the other genotypes. Prolactin hormone gene can use as a genetic marker for reproductive traits (Bai et al., 2019; Basumatary et al., 2019). The C359A polymorphism was reported in Khaki Campbell duck as being associated with egg production at 300 days, with ducks with the GT genotype producing a greater number of eggs than those with TT and GG genotypes (Chuekwon and Boonlum, 2017).

RFLP characterization analysis results by using the *Dra*I enzyme on the exon 5 *PRL* gene fragment resulted that four Egyptian duck breed *PRL* gene exon 5 at 10-weeks-body-old weight had two alleles (G and C) and three genotypes GG, GC, CC, ducks that had high frequency of allele C were superior at egg production compared with others. Also, the results of *PRL*/*DraI* in Bayang ducks resulted three genotypes consisting of homozygotes (CC), heterozygotes (CT) and homozygotes (TT) with frequencies of 0.684, 0.293 and 0.21, respectively. The proportion of alleles obtained in the Prolactin (*PRL*|*Xba*I) gene fragments in the Bayang duck studied has a frequency of genotype and allele not much different from the genotype and allele frequency values in the study of Shaoxing local Chinese ducks (Yurnalis et al., 2019). These are in accordance with present results. The different distribution of genotypes in different duck populations may be described to the different genetic background of these populations (Wang et al., 2011). Since the chicken *PRL* gene had been cloned and sequenced (Watahikiet al., 1989), most research focused on polymorphism detection in this gene.

For genetic polymorphism of PRL gene, comprising the promoter, exon 1, part of intron 1 and exon 5, the genomic sequence comparisons between four Egyptian duck breeds *PRL* gene exon 1 sequence revealed that Moulard-1 breed sample shared high similarity (100%) with Campbell-2, (99.28%) with Pekin and (97.36%) with Moulard-2, Campbell-1 and Muscovy breed samples. As Muscovy resulted high similarity (100%) with Campbell-1 and Moulard-2, and (97.12%) with Pekin. For the *PRL* gene exon 5 the sequence comparisons revealed that Moulard-1 shared high similarity (100%) with Campbell-1, Muscovy-2, but shared similarity (97.25%) with Moulard-2, Campbell-2, Muscovy-1 and two samples of Pekin-1 and Pekin-2. Several SNPs were revealed from the both type (transition and transversion) for the two exons 1 and 5. However, the difference in genotypes between four Egyptian duck breed resulted from the presence of SNPs at T/C mutation position 378 bp in intron 1 region and A/G mutation at position 5871 bp in exon 5 region (Accession no. AB158611).

A great number of SNPs were reported in *PRL* gene for chicken. From direct sequencing and association analysis, Cui et al. (2006) got six SNPs (C-2402T, C-2161G, T-2101G, C-2062G, T-2054A and G-2040A) and a 24-bp indel (insertion-deletion) showed that the 24-bp indel was correlated to egg production and chicken

broodiness. Also, three mutations screened by Liu *et al.* (2007) (C-1607T, C-5749T and T-5821C) showed a link between different haplotypes and production of eggs. In geese, three SNPs (A-401G, G-268A and T-266A) were screened in the 5′-proximal region of *PRL* gene and statistical analysis indicated that these polymorphisms have the potential to be used for egg production in molecular breeding (Jiang et al., 2009). All the above studies showed that *PRL* is an effective candidate gene for production eggs.

Assorted gene SNPs, concerning egg-laying traits in both chicken and geese, have been exposed, with few reviews in ducks (Kang et al., 2012; Kulibaba, 2015; Alsiddig et al., 2017; Mohamed et al., 2017; Feng et al., 2018). There was a number of new SNPs, not the 12 SNPs hit in the six native Chinese duck strains (Wang et al., 2011). These results showed that the duck *PRL* gene in these duck populations is rich in polymorphisms in these duck populations.

Sequence comparisons between genomic sequence of *PRL* gene exon 1 from the four Egyptian duck lines and from the other avian species showed that sequence alignments of Moulard allele B and Campbell allele B shared similarity (99.04%, 97.45%, 95.64%, 88.00%, 76.50%, 88.89%, 86.35% and 84.36%), Muscovy exon 1, Moulard allele A and Campbell allele A shared similarity (96.40%, 98.72%, 94.19%, 88.44%, 76.50%, 89.30%, 86.75% and 84.73%) and also, Pekin exon 1 shared similarity (98.08%, 97.02%, 95.16%, 87.56%, 76.00%, 88.48%, 85.94% and 84.00%) with *PRL* gene of *A. platyrhynchos* (Moulard duck), Muscovy duck, geese, chicken, turkey, Japanese quail, Indian peafowl, and ring-necked pheasant, respectively. Also, the sequence comparisons results of Egyptian duck breeds *PRL* gene exon 5 and the other avian species revealed that Moulard allele A, Campbell allele A, and Muscovy allele B) shared similarity (97.75%, 97.50%, 83.89%, 84.48%, 83.54%, 87.17% and 84.20%) and (Moulard allele B , Campbell allele B, Muscovy allele A and Pekin) shared similarity (100.00%, 98.75%, 85.68%, 85.75%, 85.09%, 87.96% and 86.65) with *A. platyrhynchos* (Moulard duck), goose, chicken, turkey, ring-necked pheasant, Ostrich and Indian peafowl, respectively.

The PRL gene has been cloned formerly in divergent avian species like pigeon, duck, chicken, quail, turkey and pigeon (Liu et al. 2008). Duck *PRL* was found to have sequence identity (92.0%, 91.7% and 91.4%) at the cDNA level compared to *PRL* of chicken, turkey and quail, respectively. The mature duck *PRL* has an overall similarity with a comparable region of chicken (95.5%), turkey (92.5%) and quail (95.5%) *PRL* (Kansaku et al., 2005). Also, the sequence analysis of the proximal region, of duck PRL promoter, displayed a high plane of similarity to turkey and chicken PRL promoter. These results viewed that the mechanisms, modulating the gene expression, may be vastly conserved in avian species (Kansaku et al., 2005). Over and above, since the avian PRL gene was cloned and sequenced, most researches illuminate new polymorphic sites in this gene (Rashidi et al., 2012).

The phylogenetic tree of exons 1 and 5 for DNA *PRL* gene in the different avian species showed that the locus of four Egyptian duck was related to *PRL* gene of *A. platyrhynchos*, *A. anser* more than of *G. gallus*, *M. gallopavo*, *P. colchicus*, *S. camelus* and *P. cristatus*. This clustering based on both of nucleotide of *PRL* gene clearly showed that the phylogenetic inter-relationship among these species and is generally in agreement with the known species relationships. This tree was constructed using Mr. Bayes, employing a previously calculated gene family with multiple sequence alignment (Huelsenbeck and Ronquist, 2001; Siltberg and Liberles, 2002).

CONCLUSION

The results of this study manipulating the four Egyptian duck breeds; Campbell, Moulard, Muscovy and Pekin, supported previous findings. That there are many SNPs found in the sequences in the four Egyptian duck breeds. The utmost vital ones, are those found at the restriction sites of *Xba*I, for the amplified fragment contained the promotor, exon 1 and intron 1 (T378C), and exon 5/*Dra*I (A5871G). These data could serve as a basis for further insight into this avian gene. Owing to the fact that the genotypes distribution in this studied between the four Egyptian duck breeds was not in Hardy–Weinberg equilibrium, to confirm the observed associations, further research should be applied to a broad and more homogeneous population of ducks. In addition, a survival evaluation and post slaughter examination of ducks must be carried out to ascertain any potential connections with polymorphic variants in the PRL gene present in duck.

DECLARATIONS

Acknowledgements

The authors sincere gratefulness to the Nubaria experimental farm, for kind assistance in collecting the blood samples of the duck breeds understudy, needed for accomplishment of this research.

Authors' contributions

All authors contributed evenly throughout the manuscript. All authors participated equally in the study plan and design. EME, NMS, DMM and MAM collected the samples from different locations and isolated the nucleic acids. NMS, DMM and MAM carried out PCR and sequencing analyses. NMS, DMM, MAM and KFM carried out the statistical analysis of data and reported the results of the molecular analysis. KFM, NMS and MAM collaborated on writing, revising, and improvement of the article for publication. All authors read and approved the final.

Competing interests

The authors declare that they don't have any conflict of interest.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication
J. World Poult. Res. 10(4): 599-604, December 25, 2020
Research Paper, PII: S2322455X2000068-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.68

The Effect of Anchovy Fish Supplementation on the Level of N-3 LC-PUFA in Egg Yolk

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Received: 25 Oct. 2020
Accepted: 09 Dec. 2020

ABSTRACT

Since the recommended daily intake of n-3 LC-PUFA is rarely met, interest in food enrichment has been increasing. It is known that dietary supplementation could alter the level and type of PUFA in the egg. Hence, the present study focused on the enrichment of egg yolk by the addition of 10% anchovy fish to the chicken diet. Based on gas chromatography analysis, dried and pre-dried anchovy from Indonesia contained a considerable amount of total eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), which was 60.10 g and 68.80 mg/100 g, respectively. After 24 days of anchovy supplementation, DHA-rich anchovy fish oil diet caused a significant increase of DHA but not EPA in egg yolk. Hens fed with anchovy could produce eggs with a higher amount of total EPA and DHA, which was up to 155.98-201.53%, as compared to control eggs. Furthermore, the sensory profile of control and enriched eggs was also evaluated. There was no significant difference in texture, aroma, flavor, and appearance between control and enriched eggs. In conclusion, this study indicated that anchovy fish supplementation could increase the level of EPA and DHA in egg yolk without causing any sensory changes in the yolk.

Keywords: Anchovy, DHA, Egg yolk, Enrichment, EPA

INTRODUCTION

Recent nutritional trends show that interest in enriched food products with omega-3 polyunsaturated fatty acids (n-3 PUFA) has been increasing. Due to their biological effects, long chain (LC) n-3 PUFAs such as eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) have gained more attention than the shorter chain n-3 PUFA α-linolenic acid (ALA). Adequate consumption of EPA and DHA has been proven to provide various health benefits, including the promotion of visual and neural development in fetus and young children, the reduction of cardiovascular disease and the attenuation of inflammation and some cancers (Lemahieu et al., 2015). Although proven to be beneficial for health, the amount of EPA and DHA obtained from the conversion of ALA in human body is not efficient. Hence, human needs to obtain n-3 LC-PUFA through their diet (Komprada, 2012).

Fatty fishes and chicken eggs are known to be rich in n-3 LC-PUFA. Atlantic salmon, which is known as gold standard for omega-3 fatty acid, contains 0.321% EPA and 1.115% DHA (FDC ID: 173686, USDA). Meanwhile, European raw anchovy contains 0.538% EPA and 0.911% DHA (FDC ID: 174182, USDA) (USDA, 2020). Even with the low-fat content, white fish such as milkfish was reported to have 0.36% EPA and 1.17% DHA (Sugata et al., 2019). Although fishes are rich in n-3 LC-PUFA, they are not consumed as much as eggs. Eggs are usually consumed as food or used as food ingredient. Thus, as compared to the fishes, eggs enriched with n-3 LC-PUFA could be one of the best options to fulfil the recommended daily intake of n-3 LC-PUFA.

Each chicken egg commonly contains 1.5 mg of EPA and 47.5 – 51.0 mg of DHA (Kovalcuks, 2014). Based on Food Data Central (USDA), every 100 g of egg yolk contains 11 mg EPA and 114 mg DHA (FDC ID: 783929). However, various feeding strategies have been applied to increase the level of PUFA in eggs. Egg yolk composition, such as EPA and DHA content, is closely

To cite this paper: Sugata M, Atmadja A, Darmawan A, Tatulus Y, Djojo SC, Rizkinata D, Rosa D, Victor H and Jan TT (2020). The Effect of Anchovy Fish Supplementation on the Level of N-3 LC-PUFA in Egg Yolk. *J. World Poult. Res.*, 10 (4): 599-604. DOI: https://dx.doi.org/10.36380/jwpr.2020.68

related to the lipids consumed by the laying hens. Enrichment of eggs with different sources of n-3 PUFA such as DHA-rich microalgae (Ao et al., 2015), ALA-rich flaxseed (Ehr et al., 2017), and DHA-rich fish oil (Lawlor et al., 2010) has been widely investigated. Previous study had been reported that ALA in plants, such as flaxseed, was effective to increase linolenic acid (LNA, 18:3 n-3) in eggs, but not EPA and DHA (Ehr et al., 2017). Meanwhile, fish oil could enrich both EPA and DHA levels in eggs (Ao et al., 2015). However, Bruneel et al. (2013) found that enrichment of eggs with n-3 PUFA could increase the level of DHA, but it was not effective on EPA level.

The most of n-3 PUFA sources used in previous studies had relatively expensive prices and were difficult to obtain in Indonesia, hence, the use of those ingredients for this study is not feasible. Indonesia is an agricultural country with high amount of fish production. In 2017, the production of anchovy fish, which is known as "ikan teri", in Indonesia reached about 3% of the world production of anchovy (MMAFRI, 2018). Moreover, to the best of authors' knowledge, enrichment of egg yolk with anchovy fish as n-3 PUFA source has not been widely studied. Therefore, this research aimed to investigate the effect of anchovy fish supplementation on the level of n-3 LC-PUFA in egg yolk.

MATERIALS AND METHODS

Source of n-3 Polyunsaturated Fatty Acids

Indonesian anchovy used in this study was *Stolephorus* sp. (based on certification from Indonesian Institute of Sciences). There were two kinds of anchovy obtained from the market: dried and fresh. Dried anchovy was fresh anchovy that had been dried before reached the market, hereinafter referred to as dried anchovy. Meanwhile, fresh anchovy was raw anchovy that was available in the market without going through the drying process. Prior to experiment, fresh anchovy was sun-dried, hereinafter referred to as pre-dried anchovy.

Lipid extraction from anchovy fish

To analyze n-3 PUFA levels, the lipid fraction of anchovy was extracted according to Bligh and Dyer (1959). One hundred gram of dried anchovy was homogenized with chloroform/methanol/water (2:2:1.8, v/v/v) as solvents. The mixture was then filtrated and centrifuged at 1000 rpm for 10 min. The lipid fraction was collected from chloroform layer at the bottom and then filtered. Afterwards, the solvents were evaporated at 50°C with agitation at 120 rpm. The lipid fraction must be converted to methyl esters (FAME) prior to analysis using gas chromatography (Harynuk et al., 2006). Fifteen milligrams of fish oil were methylated with one ml of 14% BF3-MeOH in boiling water for 7 min. After cooling, hexane (1 ml) and water were added to the mixture, followed by vigorous shaking. Phase layers would be formed, and FAMEs can be found in hexane layer on the top.

Animals' diets and egg collection

Prior to experiment, nine laying hens (28 weeks of age, Hisex Brown) from Rizky Farm (Bogor, Indonesia) were fed with commercial chicken feed. The laying hens were placed individually in cage without any environmental control and divided into three groups of three hens. The control group continued to receive 120 g commercial feed per day, while the treated groups received the commercial feed supplemented with anchovy fish (10% w/w). In other word, treated group received a mixture of 12 g anchovy fish and 108 g commercial feed every day (total feed: 120 g). The group of hens fed with dried anchovy hereinafter referred to as treatment group A, while another group fed with pre-dried anchovy hereinafter referred to as treatment group B. Feed and water were given ad libitum. For each group, laid eggs were collected at either day 20-21 (almost the end of supplementation period) and at either day 23-24 (end of supplementation period). All collected eggs were stored at 4°C until analysis.

Lipid extraction from chicken egg yolk

The extraction of lipid fraction from egg yolk was carried out according to Kovalcuks (2014). One part of egg yolk was added with two part of the mixture of hexane and isopropanol (70:30). The mixture was homogenized using a magnetic stirrer for 30 minutes at room temperature and then filtered using Whatmann filter paper number 1. The solvent was evaporated using a rotary evaporator at 80°C and a speed of 30 rpm. The lipid fraction was then methylated prior to analysis using gas chromatography. A modified method by Morrison and Smith (1964) was used to form methyl esters fatty acid (FAME) from egg yolk lipid. Twenty-five microliters of lipid were methylated with 2 ml of BF3-MeOH 14% at 60°C for 10 minutes. Water (1 ml) was added to the solution, and then FAMEs were extracted with hexane (1 ml). FAMEs were then dried over sulfate anhydrous.

N-3 Polyunsaturated Fatty Acids in anchovy and egg yolk

FAMEs were analyzed by gas chromatography (Agilent 7890A Series GC System) equipped with a 5975C Mass Selective Detector. The separation was performed on a fused-silica capillary column (0.25 µm; 30 m x 0.25 mm i.d.; DB-wax; Agilent Technologies, USA). The flow rate of the helium carrier gas was 2,69 ml/ min. The injection was operated in pulsed splitless mode at a temperature of 260°C, while the detector was set at 280°C. For analysis, one microliter of FAME was automatically injected (Agilent 7693, Agilent Technologies, USA). The column oven was set to maintain a temperature of 50°C for 1 min, then risen 25°C/ min to 200°C, and 2°C/ min to 250°C, followed by a plateau of 250°C for 20 min. The mass spectrometer was operated in selected ion monitoring (SIM) mode.

Preparation of Sensory evaluation

Thirty volunteers were involved in consumer acceptance test to assess the difference between control and enriched eggs after hard-boiled. Eggs were placed in boiling water for 10 min. After cooled, shells were removed, and each egg cut into quarters. No salt was used. There were four categories for the assessment, including appearance, texture, flavor, and aroma, which scored based on hedonic scale (1-extremely disliked; 6- extremely liked). Appearance was specified to the color of egg yolk, assuming more lipid content would give thicker yolk color, which was considered as more attractive. Texture was defined as the overall measure of oral sensations associated with placing food in the mouth. Flavor was emphasized at the savory degree of the egg, assuming higher oil content would give tastier flavor. Aroma was referred to the presence of "fishy" odor, meaning less preference in aroma indicates more "fishy" odor from the sample.

Sensory evaluation methodology

Each panelist was given two hard-boiled eggs, the first one was the control egg and the other one was the enriched egg. Both control and enriched egg were blind-coded. Each panelist was asked to evaluate these blind-coded eggs by giving a hedonic scale. Assessment was calculated by the following: Σ (number of responses × hedonic scale) / total panelist, with total number of all responses = total panelist.

Statistical analysis

The results were statistically analyzed using Minitab 15 (Minitab Inc., USA) software. All data were stated as the mean ± Standard Deviation (SD) with statistical significance at $p < 0.05$.

RESULTS AND DISCUSSION

The productive age of laying hens ranges from 28 to 97 weeks and the weight of egg yolk produced could increase with the age of hens. In general, the weight of egg yolk increases proportionally to its total lipid content (Ahn et al., 1997). However, Lawlor et al. (2010) reported that the addition of microencapsulated fish oil (20 g/kg) in chicken diet could decrease the weight of egg yolk by 5.29%. Since the consumption of n-3 LC-PUFA might decrease serum triglycerides in the hens, less lipids are available for yolk formation (Fraeye et al., 2012).

Dried anchovy contained approximately 3.33–3.59% lipid, meaning there was 0.40–0.43 g lipid in 12 g anchovy (10% w/w supplementation). Thus, the percentage of additional lipid for treatment groups was approximately 0.33–0.36% (in 120 g chicken feed). According to Khosravinia et al. (2014), adding too much fish oils to chicken feed could increase the concentration of urea and uric acid in chickens. Through the addition of 2% fish oil, Lawlor et al. (2010) reported that DHA content in chicken eggs could be increased by 54.48%. Meanwhile, Lemahieu et al. (2015) showed that supplementation of 0.68 % fish oil resulted in enrichment efficiency of n-3 LC-PUFA of more than 55%.

The results of this study showed that anchovy contained more DHA than EPA. According to Codabaccus et al. (2012), fatty fishes tend to use dietary EPA for β-oxidation, but not DHA. This might explain why EPA was not present in excess, while DHA can be found at a relatively high level in anchovy. The level of total EPA and DHA in dried and pre-dried anchovy was 60.10 and 68.80 mg/100 g, respectively. Dried anchovy was already in dried form when it was on the market; hence, the fish might have been stored for some time. On the other hand, pre-dried anchovy was still fresh when it was on the market and was dried immediately without long storage period. Crypian et al. (2017) reported that the level of PUFAs could decrease during storage because PUFAs are highly susceptible to oxidation. This might also the case with dried anchovy.

After anchovy supplementation, n-3 LC-PUFA in egg yolks was examined using GC-MS. Table 1 shows that daily enrichment with 0.33–0.36% anchovy fish oil increased the level of EPA and DHA in egg yolk, but only DHA content increased significantly ($p < 0.05$). In the end of supplementation period, the addition of dried and pre-dried anchovy increased EPA and DHA in egg yolk by 155.98% and 201.53%, respectively. Since total EPA and DHA content in pre-dried anchovy was higher than dried anchovy, it was expected that treatment group B produced eggs with higher increase of total EPA and DHA as compared to treatment group A. Other studies reported that the addition of 2% fish oil in chicken diet could increase the DHA content in eggs by 64% (Lawlor et al., 2010) or up to 300% (Gonzalez-Esquerra and Leeson, 2001). In accordance with Lawlor et al. (2010), EPA-rich and DHA-rich fish oil diet caused significant increase ($p < 0.05$) of DHA, but not EPA, in egg yolk. Since most EPA is converted to DHA before it is deposited, the major n-3 LC-PUFA in eggs is DHA (Cachaldora et al., 2008).

Table 1. The increase of EPA and DHA in the chicken eggs at the start (day 1) and at the end (day 23-24) of supplementation period

Day	Description	Yolk weight (g/egg)	Total lipid (g/egg)	Increase of DHA content per egg (%)	Increase of EPA content per egg (%)	Increase of total EPA+DHA (%)
0	Control	14.05 ± 0.59[a]	2.15 ± 0.43	-	-	-
20-21	Treatment group A	15.63 ± 0.87[b]	2.57 ± 0.39	70.08 ± 5.28[a]	6.31 ± 3.30[a]	65.89 ± 5.15[a]
	Treatment group B	15.43 ± 1.00[a]	2.60 ± 0.50	162.31 ± 8.05[b]	65.92 ± 7.09[b]	155.98 ± 7.85[b]
23-24	Treatment group A	14.79 ± 0.19[a]	2.18 ± 0.11	201.76 ± 7.71[c]	113.29 ± 22.53[c]	195.90 ± 7.56[c]
	Treatment group B	14.47 ± 0.32[a]	2.14 ± 0.52	213.27 ± 6.90[c]	34.55 ± 5.63[d]	201.53 ± 6.64[c]

Note: The table shows the data from eggs produced by hens fed with commercial feed (control), commercial feed supplemented with 10% dried anchovy (treatment group A), and commercial feed supplemented with 10% pre-dried anchovy (treatment group B). Day indicates the period of anchovy supplementation. Values with the different letter in the same column are significantly different ($p < 0.05$).

	Control	Treatment
Texture	4.63	4.63
Aroma	4.70	4.77
Appearance	4.80	4.90
Flavor	4.83	5.00

Figure 1. The overall assessment of control (— —) and enriched eggs (— —)

Although enrichment period showed a good correlation with the increase of n-3 LC-PUFA in egg yolk, in this study, the supplementation was limited for 24 days. Further studies need to be done to investigate the effect of longer enrichment period on the increase of EPA and DHA content in egg yolk, or even in chicken meat. Since about 60% of egg production costs comes from chicken feed, the addition of 10% anchovy will increase the feed cost. However, the price of omega-3 enriched eggs on the market is also double as compared to bulk eggs. Despite the more expensive price, modern society has high interest in food enrichment with n-3 PUFA due to its health benefits. Thus, the use of anchovy is expected to give little or no burden on chicken farmers.

N-3 LC-PUFA can be oxidized easily and give undesirable off-flavors in food products. Since fish oil supplementation could increase the level of lipid in egg yolk, higher extent of lipid oxidation might occur (Fraeye et al., 2012). The amount of lipid in the eggs is strongly correlated with the "fishy" taste and odor, hence, the amount of fish used for feeding strategies needs to be confined. Gonzalez-Esquerra and Leeson (2001) found that western consumers could not accept eggs produced

from inclusion of more than 1.5% of fish oil. In this study, to analyze the acceptance of panelist to the eggs enriched with 0.33–0.36% anchovy fish oil, sensory evaluation was done based on organoleptic profile of control and enriched eggs (Figure 1). Overall assessment on texture, aroma, flavor and appearance of both control and enriched eggs indicated that even though the panelist might not be able to distinguish between control and enriched eggs ($p \geq 0.05$), the enriched eggs were more preferred.

CONCLUSION

This study showed that the level of n-3 polyunsaturated fatty acids in egg yolk could be increased by the supplementation of anchovy fish in chicken diet. The supplementation of docosahexaenoic acid (DHA)-rich anchovy fish for 24 days in chicken diet caused significant increase of docosahexaenoic acid, but it was not effective on eicosapentaenoic acid in egg yolk. Furthermore, the evaluation of sensory profile of control and enriched eggs showed that there was no significant difference on texture, aroma, flavor and appearance between control and enriched eggs.

DECLARATIONS

Acknowledgements

This work was supported financially by the Centre for Research and Community Development (LPPM), Universitas Pelita Harapan (P-025-FaST-I-2019). The authors would like to thank the Biology Department of Universitas Pelita Harapan for allowing us to conduct this research in the Advanced (407) and Fundamental Biology Laboratory (202). The authors also acknowledge with much appreciation the support given by Rizky Farm.

Competing interests

The authors have declared that no competing interest exists.

Authors' contributions

TTJ formulated the concepts. AA, AD, YT and SCD collected the data and drafted the manuscript. DR[1] supported data collection. MS, HV and DR[2] analyzed the data and prepared the figures, tables. MS finalized the manuscript.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 605-614, December 25, 2020

Research Paper, PII: S2322455X2000069-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.69

Molecular Breeding of Three Genes Associated with Egg Production Traits in Three Strains of Chickens

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Received: 10 Nov. 2020
Accepted: 21 Dec. 2020

ABSTRACT

Breeding programs play an important role in increasing the performance of chickens. The poultry industry regards growth and reproduction as the two most economically valued characteristics for providing adequate animal proteins. Genetic variations are the basis of animal breeding. The present study was conducted on three genes, including Prolactin, 3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase (HMGCR), and Gonadotropin-Releasing Hormone Receptor (GNRHR). DNA was isolated from 48 chickens taken from three strains Lohmann Brown (17), Sinai (24), and Gimmizah (7) for Prolactin, HMGCR, and GNRHR gene amplification by using the PCR protocol. Electrophoresis was performed on the PCR products and the bands were viewed on a transilluminator. The size of the Prolactin gene, HMGCR, and GNRHR were 154, 675, and 210 bp, respectively. For the Sinai strain, five bands for Prolactin, two bands for HMGCR, and six bands for GNRHR were found while for the Lohmann Brown strain, five bands of Prolactin gene**,** three bands for HMGCR, and five bands for GNRHR were found. Regarding the Gimizah strain, two bands were found for Prolactin and GNRHR genes and there was only one band for the HMGCR gene. The Lohmann Brown strain respectively matured 13 and 91 earlier than Gimizah and Sinai strains with a higher egg number during the first 90 days.

Keywords: Breeding, Chickens, Egg production, GNRHR gene, HMGCR gene, Prolactin gene, PCR

INTRODUCTION

The Prolactin (PRL) gene promoter is highly polymorphic and has significant effects on egg quality traits in poultry (Liu et al., 2010). The PRL is a single-chain polypeptide hormone that belongs to the growth hormone family of genes and is mainly synthesized by lactotrope cells of the anterior pituitary gland of all vertebrates. The PRL gene is detected to be critical for the onset and kept of these reproductive behaviors in birds (Liu et al., 2010). Egg production is the most important feature in layers, which affects the economic benefits of poultry farmers (Wolc et al., 2011). Egg production is the most important trait in layer chickens as it directly influences the benefits of the poultry industry (Zhuang et al., 2019).

Molecular genetics studies the chemical mechanisms of inheritance, as an investigation of the biochemical nature of genetic material and its role in controlling phenotypic structures (Alameri et al., 2019).

3-Hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR) is a key enzyme for cholesterol homeostasis and catalyzes the rate-limiting step in cholesterol biosynthesis (Goldstein and Brown, 1990). The HMGCR gene directly regulates serum lipoprotein metabolism via a feedback mechanism (Goldstein and Brown, 1990). The HMGCR gene plays an important role during the growth and controls the transfer of primordial germ cells (Van Doren et al., 1998). The HMGCR is an important catalyzing enzyme, which catalyzes the product of 3-Hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) to mevalonate through four-electron oxidoreduction, which are the precursors for the generation of cholesterol in humans and are responsible for the production of ergosterol in plants, fungi, and protozoa (Istvan and Deisenhofer, 2000; Henriksen et al., 2006; Macreadie et al., 2006). Several polymorphisms have been identified in the HMGCR gene locus (Chasman et al., 2004). The HMGCR is indicated to be a logical candidate gene for

cholesterol metabolism, which is the rate-limiting enzyme in cholesterol synthesis (Xu et al., 2010). HMG-CoA reductase plays a significant role as a resident protein in the Endoplasmic Reticulum (ER) attached to the ER membrane consisting of eight transmembrane segments (Chen et al., 2012).

HMGCR gene is associated with chicken egg production (Han et al., 2014). The chicken HMGCR gene is located on chromosome Z, and also contains 20 exons and 19 introns. The HMGCR gene is important for the animal growth performance and metabolism of cholesterol. Wei et al. (2012) found that there is a relationship between the HMGCR gene and carcass traits, growth traits, and lipid profile in chickens.

Neuropeptide Y (NPY) and Gonadotrophin Releasing Hormone Receptor (GNRHR) are also two candidate genes that play an important role in physiological functions in growth, especially in reproduction processes (Fatemi et al., 2012). Two candidate genes, Gonadotropin-Releasing Hormone I (GNRH I) and Gonadotropin-Releasing Hormone II (GNRH II) play an important role in egg production in chickens (Bhattacharya et al., 2019). The GNRHR is a decapeptide released by the hypothalamus that regulates reproduction in most vertebrates. The GNRHR gene is one of the rhodopsin hormones and is expressed in the pituitary gland, the brain, and testes, spleen, and the heart (Carolsfeld et al., 2000). The GNRHR is related to the total egg production and the age of the first egg. The Gonadotropin-Releasing Hormone (GnRH) stimulates the release of gonadotropins from the pituitary gland through its receptor (Sun et al., 2001).

The production process of the avian egg is controlled by the hypothalamic-pituitary-gonadal-axis (Kuo et al., 2005). However, GNRHRs are mainly associated with the development and function of the reproductive axis in avian species (Bedecarrats et al., 2006). The GnRH binding to its receptor stimulates gonadotropin secretion from the pituitary gland and then induces the steroid production process in the gonads and egg production in chickens (Sonez et al., 2010). The GnRH and its receptor result in the appropriate growth, maturation, and maintenance of the gonads (Dunn et al., 2004). The GNRHR encoded gene is located on the long arm of chromosome number 10 and consists of 4 exons and a length of 2308 bp (NCBI).

The current experiment aimed to evaluate the reproductive traits of three chicken strains, including Lohman Brown, Sinai, and Gimmizah strains, raised in Egyptian environmental conditions. Moreover, three associated genes and related egg production traits were identified.

MATERIALS AND METHODS

Ethical approval

The present study was conducted at the Poultry Research unit (El-Bostan Farm), Department of Animal and Poultry Production, Faculty of Agriculture, Damanhour University, Damanhour, Egypt in 2018. This study was approved by the Experimental Animal Ethics Committee of the Faculty of Agriculture, Damanhour University, Egypt.

Husbandry of flocks

Three chicken strains, including Lohmann Brown (LB), Sinai (SI), and Gimmizah (GM), were raised in Egyptian environmental conditions and were selected for the reproductive traits evaluation. On the day of hatching, all chickens were permanently identified by wing banded and placed in floor incubators for the first week after hatching at a starting temperature of 33°C and then reduced by 2-3°C every week. All chickens were housed in the same room and had similar management and environmental conditions throughout the experimental period. At 18 weeks of age, the females were placed in individual laying cages (20 × 45 × 40 cm). All chickens were fed *ad libitum* on a diet containing 21% crude protein and 2.9 Kcal Metabolizable Energy (ME) /kg feed up to 6 weeks of age. They were then given a diet, containing 18% crude protein and 2.8 Kcal ME/Kg feed until they were 18 weeks old. Afterwards, they received a diet that contained 16% crude protein, 2.75 Kcal ME/Kg feed, 3.5% Ca, and 0.5% available phosphors during the egg production period. The light intensity decreased from 8-18 weeks of age to 8-10 hours, after that the light intensity increased to 16 hours per day during the laying period. The chickens were vaccinated against Newcastle Disease Virus, Gumboro, and Fowlpox diseases as recommended. At 30 weeks of age, wing vein blood samples were taken from chickens randomly from each genotype (strain).

Egg production traits

Age at Sexual Maturity (ASM) was recorded for each chicken, the period from hatching to the day of laying the first egg. The duration of laying time of the first 10 eggs and the weight (EW10) were determined as the number of days each chicken needed to give its first 10 eggs. Egg Number (EN90) and Weight (EW90) were recorded for each chicken during the first 90 days of laying. Egg Mass (EM) was measured for each chicken during the first 90 days of laying.

DNA extraction and primer design for three genes

Chicken genomic DNA was extracted from the blood samples using a Norgen Biotek kit, then quantified utilizing a spectrophotometer (pg T80, UK), and the final concentration for polymerase chain reaction (PCR) reaction was 50-100 ng/ul (Table 1). PCR primers were designed with NCBI and primers.

Table 1. Detail information for the primers of the candidate genes (GnRHR, PRL, and HMGCR) used for the polymerase chain reaction reaction.

Gene /ID	Location	Primers	Product size
GnRHR NC_006097.4 ID: 427517	Chromosome 10	F 5' CAGGGGACAGGGTGACCTA3' R 5'GAGGACCACGAGGGATGTTC3'	210 bp
PRL NC_006089.5 ID: 396453	Chromosome 2	F5'TTTAATATTGGTGGGTGAAGAGAC3' R 5'ATGCCACTGATCCTCGAAAACTC3'	154 bp
HMGCR NC_006127.4 ID: 395145	Chromosome Z	F 5'AGGGAACCTCCTGTGTTCCT3' R 5'AATGGACTTCGACTTGTGGGA3'	675 bp

GnRHR: Gonadotropin-Releasing-Hormone Receptor, PRL: Prolactin, HMGCR: 3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase, bp: base pair.

Table 2. The polymerase chain reaction program used for candidate genes.

Gene	Pre - Denaturation	Denaturation	Annealing	Extension	Final Extension
GnRHR	95 ^{o}C/ 5minutes	95 ^{o}C/ 45 seconds	59.9 ^{o}C / 30 seconds	72 ^{o}C/ 45 seconds	72 ^{o}C/ 5 minutes
PRL	95 ^{o}C/ 5minutes	95 ^{o}C/ 45 seconds	54.9 ^{o}C / 30 seconds	72 ^{o}C/ 45 seconds	72 ^{o}C/ 5 minutes
HMGCR	95 ^{o}C/ 5minutes	95 ^{o}C/ 45 seconds	60 ^{o}C / 30 seconds	72 ^{o}C/ 45 seconds	72 ^{o}C/ 5 minutes

GnRHR: Gonadotropin-Releasing-Hormone Receptor, PRL: Prolactin, HMGCR: 3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase.

Polymerase chain reaction amplification for the candidate genes

The PCR amplification was performed in 25 ul reaction volumes, containing master mix 2× PCR primers and DNA (Promega, Madison, USA). As can be seen in Table 2, the program for all genes was done in 35 cycles. The amplified PCR products were separated by electrophoresis on 1.5 % agarose in 1× Tris- Acetic – EDTA(TAE) buffer, ethidium bromide at the voltage of 70 volts for 1 hour, and then were read with UV light from the transilluminator (Nippon Genetics European Union).

Statistical analysis

The data of chickens from three strains of SI, LB, and GM strain were collected. The numbers of birds were 150, 130, and 101 from SI, LB, and GM pullets strain, respectively. Data analysis for egg production were performed using PROC GLM in SAS (2004) and the following formula.

$$Y_{ij} = \mu + S_j + e_{ij}$$

Where, Y_{ij} denotes observation, μ refers to general mean, Sj is the effect of strain, and e_{ij} counts for random error. The student Newman keuls option was used to test the differences between the strains. In the current experiment, ANOVA test was used to find out the significance of the experiment results. In other words, the test helps to figure out whether the null hypothesis needs to be rejected or the alternate hypothesis can be accepted under probability ($p \leq 0.01$).

RESULTS

The egg production

The least-square means for egg production traits in the three strains of Lohmann Brown (LB), Gimmizah (GM), and Sinai (SI) are indicated in Table 3. The LB strain matured significantly younger ($p \leq 0.01$) (in 147.5 days) than those of local GM and SI strains (Table 3). In addition, Sinai pullets matured earlier (in 156.6 days), compared to the Gimmizah strain (in 160.8 days).

Lohmann Brown Pullets matured 13.3 days and 9.1 days earlier than the GM and SI pullets, respectively. Regarding ASM, there was a difference between the three strains, possibly due to genetic makeup. In a breeding program, ASM is a very important trait as it affects the properties of egg production.

The duration of laying the first 10 eggs (DU 10) is presented in Table 3. There was a highly significant difference ($p \leq 0.01$) between the strains ranging from 13.5 to 17.3 days. The required time to lay the first 10 eggs of LB pullets is shorter than SI and GM pullets. The SI strain indicated a decreased in DU 10, compared to the GM strain by 2.18 days. The average egg weight of the first 10 eggs in the LB strain was 51.12 g, compared to 48.5 gm in the GM strain. The SI strain indicated a decrease in the average egg weight of the first 10 eggs of 42.7 g. The egg counts during the first 90 days were 62.45, 45.07, and 43.27 for the LB, GM, and SI strains, respectively (Table 3). The Lohmann Brown strain had a highly significant EN90 than the GM and SI strains. On the other hand, there was no significant difference in EN90 between GM and SI strain.

The Total mean of LB strain indicated a highly significant ($p \leq 0.01$) increase in average egg weight during the first 90 days (57.58g), compared to GM strain (53.81 g) and SI strain (48.74 g). The Gimmizah pullets had the highest egg weight, compared to the SI pullets in the first 90 days and the difference was significant ($p \leq 0.01$). Table 3 presents a highly significant difference ($p \leq 0.01$) between strains on egg mass during the first 90 days of laying. Pullets of LB strain produced significantly the largest egg mass, compared to the other pullet strain. The overall means of egg mass during the first 90 days were 3633.69, 2459.95, and 2099.19 g for LB, GM, and SI strain, respectively. The SI strain indicated a lower egg mass than the other strains.

Table 3. Least square means ± Standard Error and analysis of variance for egg production traits in three strains of Lohman Brown, Gimmizah, and Sinai

Trait \ Strain	GM	` SI	LB	ANOVA
Age & sexual maturity	160.89 ± 2.22^{A}	156.66 ± 1.01^{B}	147.50 ± 0.69^{C}	**
Duration of layingthe first10 eggs	17.30 ± 0.73^{A}	15.12 ± 0.21^{B}	13.59 ± 0.25^{C}	**
Egg weight at first 10 eggs	48.50 ± 0.59^{B}	42.74 ± 0.42^{C}	51.12 ± 0.32^{A}	**
Egg number during first 90 days of laying	45.07 ± 2.53^{B}	43.27 ± 0.84^{B}	62.45 ± 1.18^{A}	**
Egg weight at first 90 days of laying	53.81 ± 0.81^{B}	48.74 ± 0.79^{C}	57.58 ± 0.53^{A}	**
Egg mass	2459.95 ± 156.80^{B}	2099.19 ± 47.88^{C}	3633.69 ± 87.09^{A}	**

Different letters in each row mean significant differences ($p \leq 0.05$). **: significantly different between strains at ($p \leq 0.001$). GM: Gimmizah, SI: Sinai, LB: Lohman Brownç

Polymerase chain reaction amplification for Prolactin gene

The Prolactin gene located on Chromosome 2 is the candidate gene associated with increased egg production in chickens. The Polymerase Chain Reaction (PCR) was used to amplify the Prolactin gene fragments. The amplified product was 154 bp, indicating that the amplicon was Prolactin. For the SI strain, 5 bands appeared on lines 8, 22, 26, 64, and 70 (Figure 1). For the LB strain, five bands appeared on lines 9, 12, 14, 58, and 97 (Figure 2), and also for GM two bands appeared on lines 71 and 81 (Figure 2).

Polymerase chain reaction amplification for 3-Hydroxy-3-methylglutaryl-coenzyme A reductase gene

As an important candidate gene affecting cholesterol metabolism, polymorphisms of the HMGCR gene and their associations have attracted much attention in mammals. The amplified product was 675 bp. For the SI strain, two bands were appeared on lines 8 and 22 (Figure 3), while, three bands appeared on lines 12, 14, and 97 for the LB strain (Figure 4), finally for GM strain only one band appeared on line 81 (Figure 4).

Polymerase chain reaction amplification for Gonadotropin-Releasing Hormone Receptor gene

Fragments were amplified using PCR. The amplified product was 210 bp, indicating that the amplicon was GNRHR. For SI strain, 5 bands were displayed on lines 8, 22, 26, 64, and 71 (Figure 5). For the LB strain, 3 bands were appeared on lines 12, 14, and 97 (Figure 6). For the GM strain, 2 bands were appeared on lines 71 and 81 (Figure 6). The number of genes associated with economic characters was limited and few.

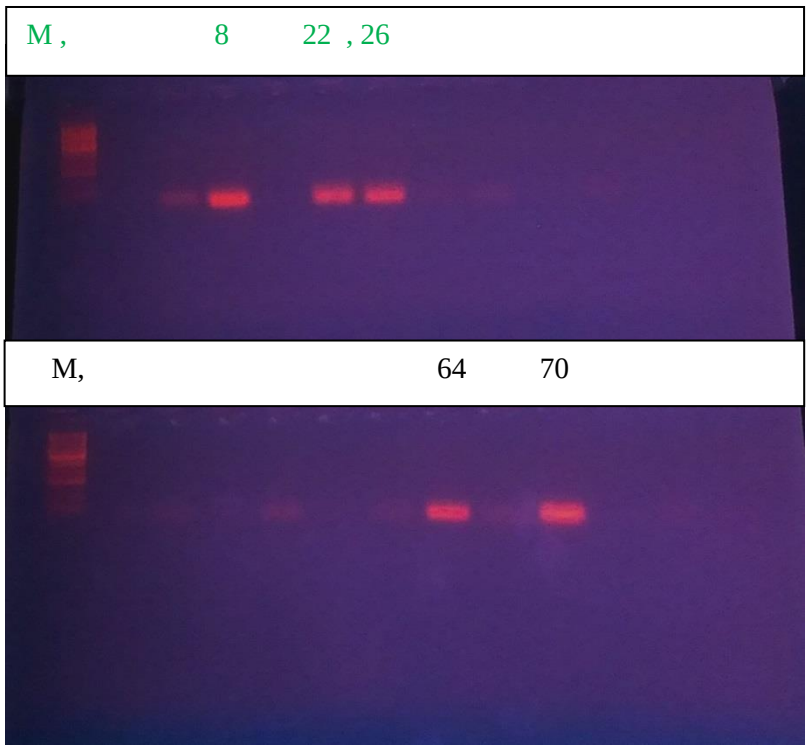

Figure 1. Polymerase chain reaction amplification gel image of the Prolactin gene of chicken (Sinai strain, M=1 kb ladder)

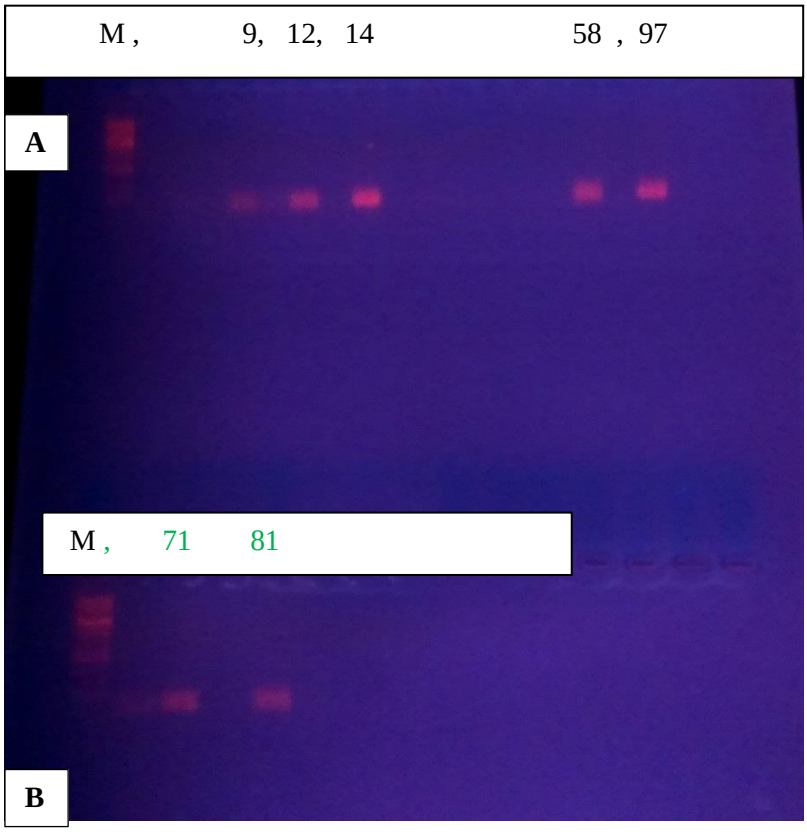

Figure 2. Polymerase chain reaction amplification gel image of the Prolactin gene of chicken (A: Lohmann Brown strain, B: Gimmizah strain, M= 100bp1kb ladder)

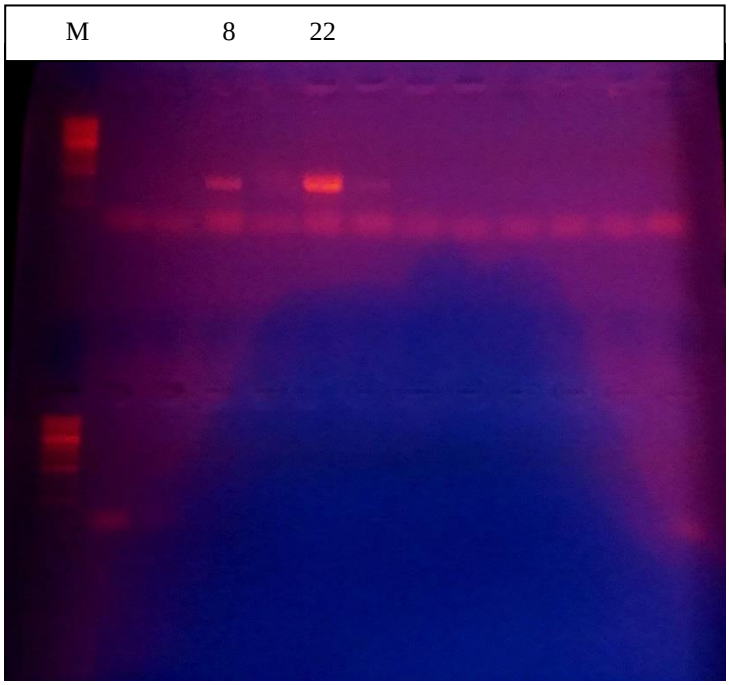

Figure 3. Polymerase chain reaction amplification gel image of the HMGCR gene of chicken (Sinai strain, M=1kb ladder)

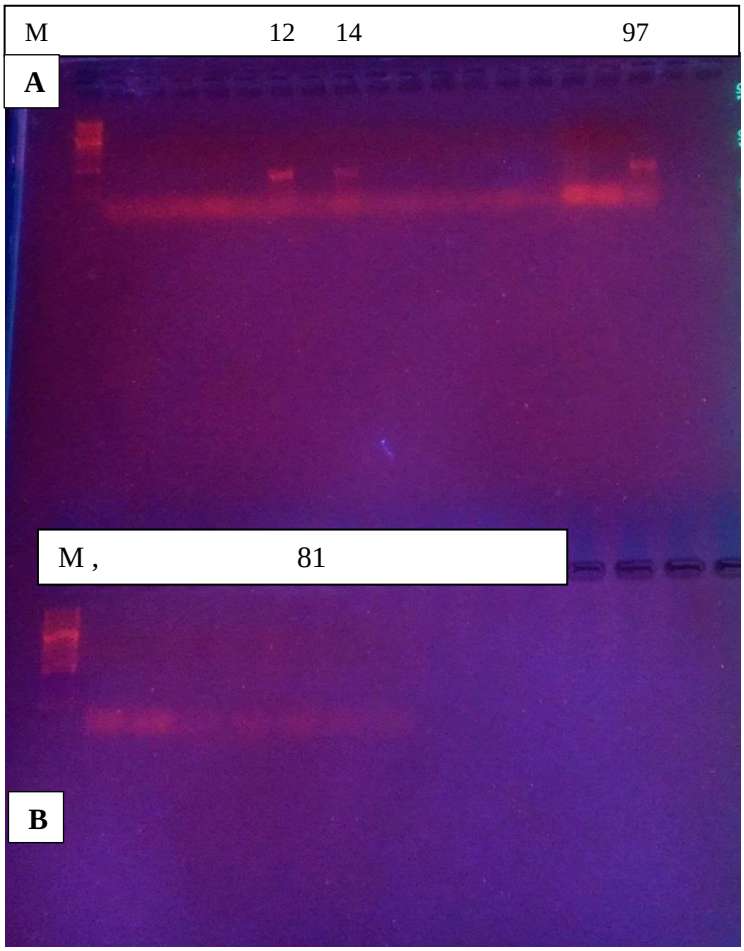

Figure 4. Polymerase chain reaction amplification gel image of the HMGCR gene of chicken. (A: Lohmann strain, B: Gimmizah strain, M= 1kb ladder)

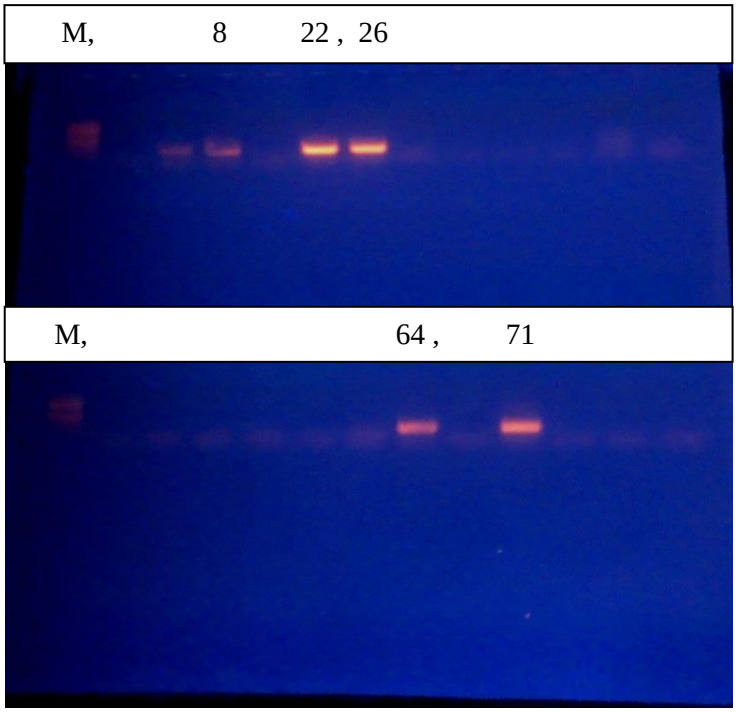

Figure 5. Polymerase chain reaction amplification gel image of the GNRHR gene of chicken (Sinai strain, M=100 bp)

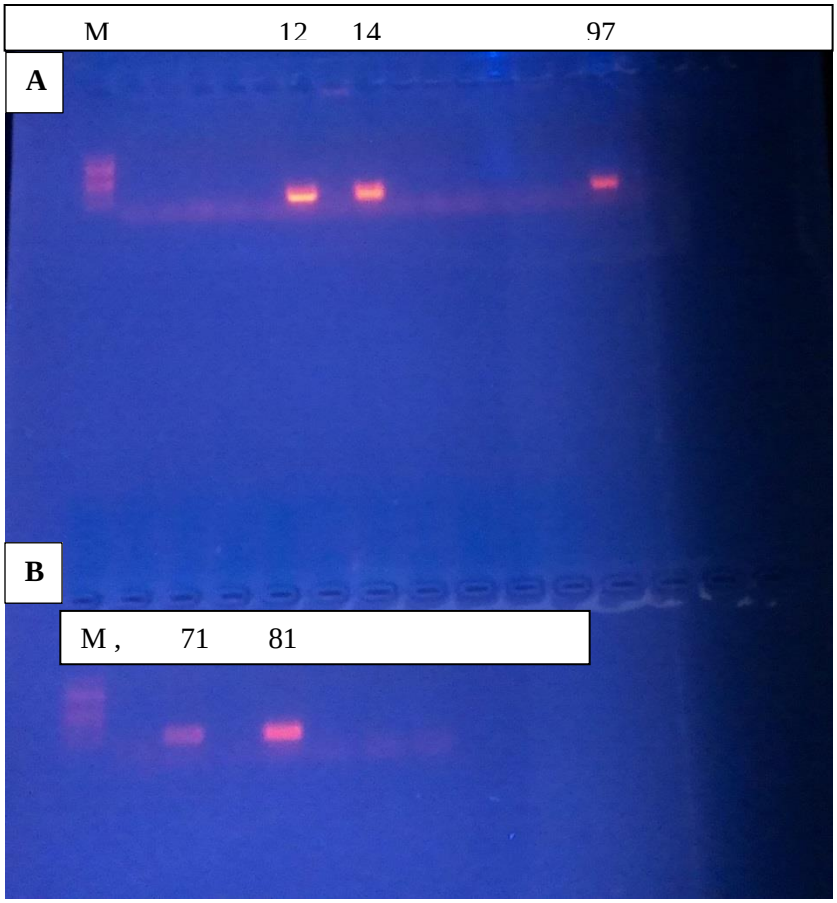

Figure 6. Polymerase chain reaction amplification gel image of the GNRHR gene of chicken (A: Lohmann Brown strain, B: Gimmizah strain, M = 100bp)

DISCUSSION

In a breeding program, ASM is a really important trait as it affects the properties of egg production. The laying duration of the first 10 eggs (DU 10) is presented in Table 3. The ASM of different strains was within the range of 13.5-17.3 days, which supported the results of studies conducted by EL-Labban et al. (2011), Ghanem et al. (2012), and EL-Tahawy (2015).

The duration of laying in the first 10 eggs (DU 10) is presented in Table 3. There was a highly significant difference ($p \leq 0.01$) between strains ranging from 13.5 to 17.3 days, which is in line with the previous studies reported by Bonekamp et al. (2010), and Taha et al. (2012). The number of eggs during the first 90 days was calculated as 62, 45, and 43 for LB, GM, and SI strains, respectively. The obtained results of maturity agreed with studies performed by Alicja Sobczak and Krzysztof, (2015), and EL-Tahawy (2015) that found the overall means of ASM 147.5 and 156.6 days for LB and SI strains, respectively. Present results in Table 3 were in agreement with those obtained by Bonekamp et al. (2010), and Alicja sobczak and Krzysztof (2015). The overall means of egg mass during the first 90 days were 3633.69, 2459.95, and 2099.19 g for LB, GM, and SI strains, respectively, which was consistent with the results reported by Soares et al. (2011), Alicja sobczak and Krzysztof (2015), and EL-Tahawy (2015).

Various studies have indicated that polymorphisms in the chicken PRL gene of different breeds are associated with egg production (Bhattacharya et al., 2011; Cui et al., 2006). Prolactin regulates important physiological functions, such as reproductive and homeostatic effects. Elkins et al. (2000), and Zhang et al. (2012) found that the polymorphism of the PRL gene was significantly associated with egg production traits in chickens and that it is a strong candidate gene affecting egg production traits.

The HMGCR was considered to be a logical candidate gene for cholesterol metabolism, as HMGCR is the rate-limiting enzyme in cholesterol synthesis (XU et al., 2010). The GNRHs are responsible for the development and function of the reproductive properties in avian (Bedecarrats et al., 2006).

CONCLUSION

In a breeding program, age at sexual maturity (ASM) is a very important trait as it affects the properties of egg production. Based on the obtained results of the current study, ASM was significantly different among the three strains of Lohmann Brown, Sinai, and Gimmizah possibly due to the genetic makeup. The Lohmann Brown strain can be used to mature earlier and have a higher egg number than Gimizah and Sinai strains during the first 90 days. The performed PCR indicated some bands for Prolactin, 3-Hydroxy-3-methylglutaryl-coenzyme A reductase, and Gonadotrophin Releasing Hormone Receptor genes. The authors of the present study aim to complete their works by examining gene expression using RT-PCR.

DECLARATION

Authors' contribution

El-Tahawy collected the samples and designed research. Abdel-Rahman was responsible for DNA extraction, PCR, and participated in writing. All authors checked and confirmed the final draft of manuscript.

Acknowledgments

Research supported by the Science and Technology Development Fund (STDF, 2418).

Competing interests

The authors of present study did not have any conflict of interests.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 615-622, December 25, 2020

Research Paper, PII: S2322455X2000070-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.70

The Effect of Dietary Administration of Virgin Coconut oil on Differential Leukocytes in Infected Chicken with *Eimeria tenella*

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Received: 03 Nov. 2020
Accepted: 18 Dec. 2020

ABSTRACT

Coccidiosis is the main problem in poultry diseases. It is caused by the parasite *Eimeria tenella,* which induce the immune response of leukocyte. Anticoccidial drugs are administered in the poultry feed to control coccidiosis. However, taking medication for a long time can lead to resistance. Recent studies have indicated that Virgin Coconut Oil (VCO) has some benefits, including anti-inflammatory effects. The present research aimed to identify the effect of VCO at the different doses in improving the various leukocyte counts of chickens infected with *E. tenella*. Male chickens were divided into five groups (T0, T1, T2, T3, and T4) and treated for 28 days. T0 was neither infected with *E. tenella* nor get treatment, T1 was only infected with *E. tenella*, T2 was treated with 5 ml/kg VCO feed and had *E. tenella* infection, T3 was treated with 10 ml/kg VCO feed and had *E. tenella* infection, and T4 was treated 20ml/kg VCO feed and had *E. tenella* infection. Differential leukocyte was counted with a blood cell counter. The data obtained were analyzed using ANOVA and Duncan's Multiple Range Test. The results indicated that a dose of 10 ml/kg feed and 20ml/kg feed of VCO could improve the differential leukocyte counts of chickens infected with *E. tenella* by maintaining the counts of basophil, eosinophil, heterophil, monocyte, and lymphocyte in the normal range. The present study concluded that VCO by a dose of more than 10 ml/kg would improve the differential leukocyte counts of chickens infected with *E. tenella*.

Keywords: Differential leukocyte count, *Eimeria tenella*, Virgin Coconut Oil

INTRODUCTION

Coccidiosis caused by the parasite *Eimeria tenella* is the main problem facing poultry farmers. This parasite has a high virulence and multiplies intracellularly in the digestive tract of chicken caecum (Habibi et al., 2016; Fatoba and Adeleke, 2018). Coccidiosis is a disease caused by protozoa in a phylum of Aplicomplexa and genus *Eimeria*. Coccidiosis causes damage to the gastrointestinal tract and primarily affects domestic animals, wild animals, and poultry (Debbou-Iouknane et al., 2018; Dubey, 2018; Bachene et al., 2019). Although coccidiosis is a disease that was recognized long ago, the impact of economic loss because of it causing coccidiosis is becoming an important issue in society (Chapman, 2008; Debbou-Iouknane et al., 2018).

The economic loss caused each year by the coccidiosis in a poultry industry around the world reaches about US$ one billion, due to the decrease in poultry performance and an increase in production cost (Berezin et al., 2010). Seven species of *Eimeria* (*E. acervulina, E. brunetti, E. maxima, E. mitis, E. nectrix, E. praecox,* and *E. tenella*) were known to be pathogenic in chickens (Chengat Prakashbabu et al., 2017), Among all *Eimeria* species, however, *E. tenella* is the most pathogenic species in which the predilection lies in the caecum and causes caecal coccidiosis (Muazu et al., 2008). Coccidiosis is controlled by adding anticoccidia to the feed (Pop et al., 2019). Recently, the usage of anticoccidia is still the main choice in the poultry industry as drugs administration is more effective than just depending on the poultry immune response (Alfaro et al., 2007; Pop et al., 2019). However, regular using of anticoccidial drugs over a long period of time had caused coccidian to become resistance to the drug, so the use of anti-coccidia and antibiotics must be reduced (Tipu et al., 2002).

There is a specific system in the body to eradicate various infectious and toxic materials. So, the immune system consisted of leukocyte (white blood cells) and tissue cells that derive from leukocyte. A disruption of the immune system leads to a change in the immune function,

especially the cellular immune system such as leukocyte (Roeslan, 1996). Therefore, the leukocyte count of calculations can be used as one of the immune response indicators to determine if there is an infection in the body (Abdul Mohymen et al., 2014).

Virgin Coconut Oil (VCO) is a dietary supplement which can be produced by Indonesian coconut farmers in the home industry and is proved secure to be consumed by a human. Hence, it is believed that VCO can also be useful as a feed additive to be consumed by chickens (Attia et al., 2020). Recent studies have shown those VCO exhibits varying degrees of beneficial properties, such as antiviral, antibacterial, antifungal, anti-inflammatory, antipyretic, and antioxidant properties (Akinnuga et al., 2014). Virgin Coconut Oil (VCO) has proven to have a broad spectrum of antimicrobial activities against pathogenic microorganisms, including Gram-positive bacteria, i.e. *S.aureus*, *Listeria monocytogenes*, *Streptococcus pyogenes*, and *Bacillus cereus*; Gram-negative bacteria, i.e., *Escherichia coli*, *Vibrio cholera* and *Salmonella* Typhi and yeast, i.e. *Candida albicans*, *C.krusei* and *Pityrosporumovale* (Long, 1968).

In addition, a recent study on the effect of VCO against coccidiosis in broiler chicken indicated promising results and could be used as an alternative method to control coccidiosis in the poultry industry (Tan and Long, 2012). So, the objective of the present study was to evaluate the effect of VCO in improving the differential leukocyte count of broiler chicken infected with *E. tenella*.

MATERIALS AND METHODS

The present research used some equipment. There was chicken cage, feed and drink media, label, scale, media for gems, Slide, microscope, syringe, beaker glass, spuit, petri dish, cover dish, centrifuge, pipet, cover glass, and Blood Cell Counter.

The present research used *Eimeria tenella* from the Parasitology Department of Universitas Airlangga, DOC (Day Old Chick) strain Cobb from the chicken supplier in Surabaya, 14 days old chicken with Specific Antibody Negative (SAN), potassium dichromate (K2Cr2O7) 2.5%, sugar solution 96%, equates, Giemsa 10%, distilled water, methanol and Virgin Coconut Oil (VCO) from Vico Bagoes by dr. Zainal Gani Jakarta.

Ethical Approval

Ethical regulations in the present study from the perspective of an animal breeder and researcher (chicken cage, feed drink media and handlings) were in according to "Bioethics of Poultry Production" (Macer, 2019).

Activation and multiplication of *Eimeria tenella* oocysts

Eimeria tenella isolate was activated by infecting five chickens at the age of two weeks that had never been infected by coccidiosis with 10,000 doses each. The chicken feces were collected on the seventh day after infection until the chickens were slaughtered on day tenth day. The feces were then mixed and placed in 2.5% potassium dichromate (K2Cr2O7) medium at room temperature (28° C) for 24-48 hours for the sporulation process, so that the infectous oocysts of *E. tenella* were obtained.

The sugar solution was mixed with the feces that has been speculated in the 2.5% potassium dichromate and placed in a beaker glass at the ratio of 1/1. The solution was stirred until completely homogenous and then poured into a petri dish. After five minutes and the oocysts rose to the surface, the petri dish closed with the cover dish. After 30 minutes cover dish was lifted and washed with equivalents including distilled water. The oocyst suspension was then poured into a beaker glass. The isolation was done 5 to 6 times. The oocyst suspension, which still contained sugar, was washed with distilled water and centrifuged at 2500 rpm for 5 to 10 minutes. This process was performed 3-4 times until the oocyst suspension became clear.

The oocysts count was performed using Haemositometer-Improved-Neubauer. The oocysts were observed and calculated under a microscope with 100× magnification. The calculation was made from the oocysts on four large squares in the corner of the courtroom. The number of oocysts from each milliliter suspension was therefore 2.5 × 1000 n = 2500 n. The desired infection dose was prepared by diluting, so that each milliliter contained the required number of oocysts.

Treatment of chickens

The experimental unit that was used in the present study was healthy male Day-Old Chickens (DOCs) from a chicken supplier in Surabaya. The chickens' diets were standard feed for starter (0 to 7 days) and grower (8 to 34 days) diets, without coccidiostats additive (Tan and Long, 2012).

Samples of 30 DOCs were divided into five groups, the controlled negative (T0) group, the control positive (T1) group, the treatment I (T2) group, the treatment II (T3) group, and the treatment III (T4) group. In the control negative (T0) group, the chicken was not infected

with *E. tenella* and was not treated with VCO. The chicken's cage was separated from the control positive (T1) group and treatment (T2, T3, and T4). In the control positive (T1) group the chicken was only infected with *E. tenella* at the age of 21 days old but was not treated with VCO. In the group of treatment I (T2), the chicken was treated with five ml VCO/kg feed from one day old chicken up to 28 days and infected with *E. tenella* at the age of 21 days old. In the group of treatment II (T3), the chicken was treated with 10 ml VCO/kg feed from one-day old chick up to 28 days and infected with *E. tenella* at the age of 21 days old. In the group of treatment III (T4), the group was treated with 20 ml VCO/kg feed from one-day old chick up to 28 days and infected with *E. tenella* at the age of 21 days.

Blood sampling and smear preparation

Blood sampling was done on hatch day, day three, and day six after infection. The blood was taken from the brachialis vein and then the blood smear was prepared. One drop of the chicken blood sample was anticoagulant in the first slide with a flat position. Then, the slide with blood sample was shifted using another sterile slide with an angel of 30° so that it formed a thin layer of blood and it was dried at environment temperature. The blood smear was then soaked into methanol as a fixation within five minutes. The blood smear was dried at the environment temperature and then soaks into gems stain for 30 minutes. Thereafter, the blood smear was washed with water after staining, then the blood smear was placed vertically and allowed to dry again. Then a drop of Immersion oil was dropped on the blood smear and was observed under a microscope with 1000× magnification. The count started in the count area from the top left to bottom, then shifted to the right and then to the up and repeated until 100 cells of leukocyte were gotten based on the types using blood cell counter.

Data analysis

The design of the present research used completely randomized design. The data were analyzed by analysis of variance (ANOVA) and then followed by Duncan's Multiple Range Test to compare the treatment effect of each treatment.

RESULTS

The leukocytes count in each treatment group was performed from the blood smear. These five distinct leukocytes were basophil, eosinophil, heterophil, monocyte, and lymphocyte. The data on the leukocyte count were given as follows. The results of basophil count from the blood smear from *E. tenella* infected chicken that had been treated with VCO are presented in table 1.

The data analysis of the VCO addition in the feed indicated that there was no significant difference ($p < 0.05$) in the basophil count. The Duncan's Multiple Range Test indicated that the infected group had the highest decreasing amount of basophil among other groups on the day 6th after infection. The 3rd day after the infection group had the highest amount of basophil count and the highest number that could have got was from the T4 group with one basophil cell. The sixth day after the infection, infected group had less amount of the basophil and the lowest number that could have got was from the T1, T3, and T4 group with no basophil cell found. The results of eosinophils count from the blood smear of chicken treated with the VCO are presented in table 2.

Table 1. The result of the basophil count of the VCO effect in chicken infected with *E. tenella*

Treatment	Day after infection		
	0	3	6
T0	$0.50^{a} \pm 1.00$	$0.50^{a} \pm 0.58$	$0.25^{a} \pm 0.50$
T1	$0.75^{a} \pm 0.96$	$0.75^{a} \pm 0.50$	$0.00^{a} \pm 0.00$
T2	$0.25^{a} \pm 0.50$	$0.50^{a} \pm 0.58$	$0.25^{a} \pm 0.50$
T3	$0.25^{a} \pm 0.50$	$0.25^{a} \pm 0.50$	$0.00^{a} \pm 0.00$
T4	$0.50^{a} \pm 0.58$	$1.00^{a} \pm 1.15$	$0.00^{a} \pm 0.00$

[a:] Means within a column with different superscripts differ significantly ($p < 0.05$). T0: negative control, T1: positive control or infected with *E. tenella*, T2: 5 ml/kg feed of VCO, T3: 10 ml/kg feed of VCO, T4: 20 ml/kg feed of VCO.

Table 2. The result of eosinophil count of the VCO effect in chicken infected with *E. tenella*

Treatment	Day after infection		
	0	3	6
T0	$2.00^{b} \pm 1.41$	$3.50^{a} \pm 2.08$	$4.25^{b} \pm 1.26$
T1	$4.25^{a} \pm 1.50$	$4.25^{a} \pm 1.25$	$6.75^{a} \pm 2.50$
T2	$4.50^{a} \pm 1.73$	$4.50^{a} \pm 1.00$	$2.50^{bc} \pm 1.29$
T3	$3.25^{ab} \pm 0.50$	$4.75^{a} \pm 2.63$	$1.00^{c} \pm 1.15$
T4	$3.50^{ab} \pm 1.29$	$4.75^{a} \pm 1.26$	$1.00^{c} \pm 0.82$

[a, b, c:] Means within a column with different superscripts differ significantly ($p < 0.05$). T0: negative control, T1: positive control or infected with *E. tenella*, T2: 5 ml/kg feed of the VCO, T3: 10 ml/kg feed of the VCO, T4: 20 ml/kg feed of the VCO.

The data in table 2 indicated that there was a significantly different ($p < 0.05$) among each group which increased in the third day and decreased in the sixth day after the infection. The third day after the infection, the infected groups which had the highest number of eosinophil were T3 and T4. Otherwise, the sixth day after the infection, the groups which had the less number of eosinophil were also T3 and T4. Although the T3 and T4

were not significantly different from each other, they significantly different from other groups. T1 group was significantly different from the T2 group on the sixth day after infection. T1 group had the highest number of eosinophil among all groups on the day six after infection. Otherwise, T3 and T4 group had the lowest number of eosinophil among all other groups on the day six after infection. The results of heterophils count from the blood smear of chicken treated VCO are presented in table 3.

The data of table 3 presented that the T3 and T4 groups were significantly different ($p < 0.05$) from all other groups, although T3 and T4 group were not significantly difference with each other. The highest number of heterophil on the third day after the infection was seen in the T2 group. The lowest number of heterophil on the sixth day after the infection was seen in the T4 group. The results of Monocytes count from the blood smear of chicken treated with the VCO are presented in table 4.

The data had a significant difference ($p < 0.05$) in the T4 group. The T1 group had the highest number of monocyte on the third day after infection, while the T4 group had the lowest number of monocyte on the third day after infection. The T4 group had the lowest number of monocyte on the sixth day after infection. The results of the lymphocyte count from the blood smear of chicken was treated with the VCO are presented in table 5.

The data of table 5 indicated significant difference ($p < 0.05$) on the sixth day after the infection. The T4 group had the highest number of lymphocyte on the sixth day after infection, while the T3 group had the lowest number. The T2 and T3 groups showed significant difference at the beginning of the trial, the third, and the sixth day after infection. Although the T4 group showed a significant difference at the beginning of the trial and on the third day after infection, did not show any significant difference on the third and sixth days after infection. T1 group or control positive group showed a constantly decreasing number of lymphocytes, in contrast to other groups which showed an increasing number of lymphocytes.

Table 3. The result of the heterophil number of VCO effect in infected chicken with *E. tenella* infected chicken

Treatment	Day after infection		
	0	3	6
T0	$13.75^{a} \pm 2.22$	$13.5^{a} \pm 2.08$	$7.75^{a} \pm 1.50$
T1	$12.00^{a} \pm 2.94$	$11.00^{a} \pm 1.63$	$7.00^{a} \pm 2.16$
T2	$13.25^{a} \pm 2.22$	$11.75^{a} \pm 1.70$	$7.75^{a} \pm 3.09$
T3	$15.25^{a} \pm 1.89$	$4.00^{b} \pm 1.41$	$10.50^{a} \pm 1.73$
T4	$13.75^{a} \pm 2.63$	$4.50^{b} \pm 2.08$	$6.75^{a} \pm 2.50$

a, b: Means within a column with different superscripts differ significantly ($p < 0.05$). T0: negative control; T1: positive control or infected with *E. tenella*; T2: 5ml/kg feed of VCO; T3: 10ml/kg feed of VCO; T4: 20ml/kg feed of VCO.

Table 4. The result of monocyte count (%) of the VCO effect in chicken infected with *E. tenella*

Treatment	Day after infection		
	0	3	6
T0	$5.50^{ab} \pm 1.91$	$5.50^{b} \pm 1.29$	$7.75^{a} \pm 1.50$
T1	$2.00^{c} \pm 0.82$	$8.25^{a} \pm 2.06$	$7.00^{a} \pm 2.16$
T2	$6.50^{ab} \pm 2.08$	$4.75^{b} \pm 1.26$	$7.75^{a} \pm 3.09$
T3	$7.75^{a} \pm 2.50$	$4.00^{b} \pm 1.41$	$10.50^{a} \pm 1.73$
T4	$4.50^{bc} \pm 1.00$	$4.50^{b} \pm 2.08$	$6.75^{a} \pm 2.50$

a, b, c: Means within a column with different superscripts differ significantly ($p < 0.05$). T0: negative control, T1: positive control or infected with *E. tenella*, T2: 5 ml/kg feed of the VCO, T3: 10 ml/kg feed of the VCO, T4: 20ml/kg feed of the VCO.

Table 5. The results of the lymphocyte count of the VCO effect in chicken infected with *E. tenella*

Treatment	Day after infection		
	0	3	6
T0	$72.00^{b} \pm 3.74$	$77.00^{a} \pm 2.70$	$79.75^{b} \pm 0.50$
T1	$80.00^{a} \pm 5.71$	$73.75^{a} \pm 2.87$	$73.75^{c} \pm 2.87$
T2	$75.50^{ab} \pm 3.78$	$78.50^{a} \pm 2.08$	$82.00^{b} \pm 2.45$
T3	$72.50^{b} \pm 4.04$	$76.75^{a} \pm 4.35$	$77.25^{bc} \pm 5.73$
T4	$77.75^{ab} \pm 0.16$	$75.25^{a} \pm 4.19$	$88.75^{a} \pm 5.93$

a,b,c: Means within a column with different superscripts differ significantly ($p < 0.05$). T0: negative control, T1: positive control or infected with *E. tenella*, T2: 5 ml/kg feed of VCO, T3: 10 ml/kg feed of VCO, T4: 20 ml/kg feed of VCO.

DISCUSSION

The average basophil count in each group was about zero to two percent or was still within the normal basophil range of one to four percent (Current et al., 1983), which proved that VCO was able to affect the amount of basophil. Basophil played the weakest role in the immune system (Tizard, 2013; Eberle and Voehringer, 2016), which is rarely found in the poultry blood under normal conditions. That is the reason for the low percentage of basophil in the total blood leukocytes.

The result also showed that the basophil increased on the third day after infection, possibly due to the fact that the basophil was stimulated at the inflammation site on the caecal epithelial caused by *E. tenella*. Basophil contains serotonin, heparin, and histamine that stimulate blood flow to the site of inflammation (Bijanti et al., 2010). Otherwise, the basophil decreased on the sixth day after infection, possibly because VCO acts as an anti-inflammation substance (Sharifi-Rad et al., 2017). Virgin coconut oil has anti-inflammatory, moderate analgesic, and antipyretic properties (Intahphuak et al., 2010). It had been shown that fatty acids such as oleic and stearic acids in VCO attenuated the activity of polymorph nuclear

leukocytes, which led to the suppression of inflammatory processes. It was suggested that the proportion of fatty acids integrated into membrane phospholipids affect membrane fluidity, which in turn could influence cell function (Zakaria et al., 2011). VCO had monolaurin and monocaprin substance, a monoglyceride substance that was used as anti-microbe, anti-viral, antibacterial, and antiprotozoal because they can dissolve the lipid-coated wall of the microbes, causing the cells of the microbes to rupture and die, so the amount of the parasites in the tissues and the amount of basophil would reduce (Arlee et al., 2013).

The data showed a significantly different ($p < 0.05$) eosinophil counts. The data showed that the T3 and T4 group had the highest amount of increasing number of eosinophil on the third day after infection. Increasing numbers of eosinophils might be due to the VCO, which could help stimulate the immune system of the chicken. Even though eosinophil is most active during helminth parasite infection, some studies stated that the coccidian parasite could also lead to eosinophilia (Nutman, 2007). On the sixth day after infection, the most decreasing amount of eosinophil was observed in the T3 and T4 group. This might be because the VCO acted as an antiprotozoal and anti-inflammation, so the number of parasites in the tissues and the amount of eosinophil would decrease.

The normal range of eosinophil in the blood is about 2-8% of the total amount of leukocytes, so the number of eosinophil in the present research was still in the normal range. Eosinophil neutralize inflammatory factor released by mast cells and basophils in type 1 hypersensitivity reaction (Tizard, 2013). Eosinophil acts as a regulator of parasite infection by attaching to the parasite and releasing toxic substances to the parasite (Wen and Rothenberg, 2016). Eosinophil regulates the allergic reaction and acute inflammation, which can stimulate tissue damages (Jain, 1993).

It was known that eosinophils interact with homocytotropic antibodies (IgE and IgG), mast cells, and basophils. The antibody and T lymphocytes provided specificity for the reaction, and the IgE on mast cells attracted eosinophils to modulate the inflammatory reaction. The relative amounts of tissue IgE, extractable histamine, and eosinophil suggested that these components form the immune system that was most pronounced on body surfaces, immunologically mediated, often parasitic related and frequently associated with eosinophilia (Ross et al., 1999).

The data in the table 3 indicate that there was a significant number of heterophilic differences ($p < 0.05$) between each day after infection, although there were still decreasing numbers of heterophil on the third and sixth days after infection. The results shown in the table 3 also announce that the average amount of heterophil tended to decrease constantly. A decrease in the amount of heterophil might be because heterophil has the opposite effect on lymphocytes called the H/ L ratio and this ratio is influenced by diseases and infection (or the stress hormones produced by infection) (Davis et al., 2008). It could also happen because VCO stimulated the host cell-mediated immune system, which was done by lymphocyte T.

Heterophiles could survive in tissues for one to two days. In the present study, however, the heterophiles decreased steadily for six days, possibly because VCO constantly helps reduce the inflammatory factors as was given to the chickens daily. Heterophile has most of the lysosomal enzymes, which are proteolytic enzymes used to digest bacteria and foreign protein materials (Guyton and Hall, 2006). Heterophiles find, digest, and kill foreign bodies and also acts as the first line of defense (Ganong and Ganong, 1995).

In table 3, the number of heterophile (8.33%-11.67%) was considered below the normal range (20.9% or 25%-30%) and reported as heteropenia. Heteropenia could be observed in the chicken infected with *E. coli* after three and six hours. Heteropenia or heterophilia in chickens could occurred with inflammation or infection, stress and sometimes neoplasia (DeRosa et al., 1992).

The data in table 4 indicate a significant difference in monocyte counts, although the T4 group had the lowest number of monocytes on the sixth day after infection, as VCO might reduce the oocyst in the chicken, which would lead to a decrease in the inflammatory factor. If the inflammatory factor is reduced, it also decreases the migration of monocytes to the caecal tissue. The reduction in the monocytes could indicate the healing process. The administration of VCO increased the secretion of thyroid hormone, which led to an increase in the metabolism process. If the metabolism increases, the cell function will be more efficient, which helps to protect the body from the bad condition and also accelerate the healing process (Boateng et al., 2016).

Monocytes are produced in the bone marrow about three to eight percent of the total leukocytes in the blood. Monocytes in poultry are the largest leukocytes with various forms from rounded to amoeboid shape. Compared to lymphocytes, the chromatin granules of the

monocyte nucleus are less accumulated. Monocytes indicated phagocytic activity and migration into the tissues to become macrophages (Bijanti et al., 2010). Apart from the macrophage, monocytes are important to maintain the immune response by releasing glycoprotein regulators/monokines such as interferon, interleukin-l, hormone-like AMP (Adenosine Monophosphate), and active pharmacological substances such as prostaglandines and leukotrienes (Tizard, 1982).

The data in table 5 reveal significantly different ($p < 0.05$) lymphocyte counts, but the group treated with VCO indicated a more constant increase in lymphocyte count than the control negative group, and the T4 group had the most lymphocytes counts. It was known that palmitate and myristate acid in VCO are the phospholipid component of T lymphocytes. Therefore, VCO could stimulate lymphocytes and produce an antibody in the chickens (Gordon, 2003).

The T lymphocyte plays an important role in stimulating the immune system against certain diseases and stress factors. The T lymphocyte would react directly to antigen presented to the cell surface by an Antigen-Presenting Cell (APC). The Th-CD4 interaction served to maintain the Th-APC binding intact during the specific antigen activation (Hussain et al., 2004). Lymphocyte Th would activate macrophages as a cellular immune response against infection with the intracellular pathogen (Gordon, 2003).

The result in table 5 shows that the T4 group had the highest lymphocyte counts, although the T3 had the lowest lymphocyte counts and the most stable increase in the lymphocyte counts. Possibly because VCO reduced the oocysts, so that the lymphocyte counts reduced. The stable increase could indicate the VCO function as an immunostimulant. The percentage range of lymphocyte count for T0-T3 was 75.5% to 82% or was still in the normal range of lymphocytes (24%-84% of total leukocytes in the blood), but the T4 group on the sixth day after the infection indicated that the lymphocytes count was more than the normal range, possibly because the stress effect of the chicken or the 20 ml/kg feed dose of VCO had too much influence on the lymphocyte T production.

Eimeria tenella infection in chicken could cause the lymphocyte counts to reach 87% or exceed the normal range. The increase in the lymphocyte count could attributed to the effect of the inflammation of the caeca-intestine (Patra et al., 2010). Chronic antigenic stimulation could lead to a greatly expanded circulating lymphocyte pool since the primary functions of the lymphocyte are immune response, humoral antibody production, and cell-mediated immunity (Jones, 1999). Cell-mediated immunity plays an important role in protecting the chicken from coccidial infection.

There is increasing evidence that cell-mediated immunity plays a major role in resistance to infection, as T lymphocytes appear to respond to coccidial infection by both cytokine production and a direct cytotoxic attack on infected cells (Lillehoj and Trout, 1996; Yun et al., 2000).

CONCLUSION

The research result proved that adding Virgin coconut oil could improve the different leukocyte counts of chicken infected with *E. tenella*. The virgin coconut oil at the dose of 10 ml/kg feed as a dietary supplementation and 20 ml/kg feed had the most significant result in improving the different leukocytes counts of the chicken infected with *E. tenella*. So, dietary ingestion of efficient vegetable oil especially Virgin coconut oil, regardless of efficient farming, could be useful in combating some parasitic diseases.

DECLARATION

Authors' contribution

All authors of manuscript; Z. Sheila Faradilla, Muchammad Yunus, and H.A. Hermadi had similar and continuous attempts *in in vivo* and *in vitro* experiments of present study.

Competing interests

The authors have declared there was no conflict of interest.

Acknowledgments

The authors thank the staff of the Faculty of Veterinary Medicine, Universitas Airlangga for supports and facilities.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 623-630, December 25, 2020

Research Paper, PII: S2322455X2000071-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.71

Characteristics of Carcass Traits and Meat Quality of Broiler Chickens Reared under Conventional and Free-range Systems

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Received: 01 Nov. 2020
Accepted: 14 Dec. 2020

ABSTRACT

Alternative chicken production systems have become popular in recent years due to animal welfare criteria and consumer's perceptions. General beliefs express that the meat quality of chicken reared under free-range systems is better than that of chickens under conventional production conditions. The aim of this study was to compare the meat quality and carcass traits of chickens raised in conventional and free-range systems. Either conventional or free-range systems used meat-type Hubbard JA57 birds with a slaughter age of approximately 78 days. For assessing carcass traits and meat quality, six male chickens were selected from each system. The meat quality parameters, pH at 45 minutes, ultimate pH, color coordinates, drip loss, cooking loss, and water-holding capacity were measured. Furthermore, proximate parameters, such as crude protein, total fat, and crude ash were determined. There were no significant differences in main carcass yield and breast muscles between chickens reared in two systems, however, color values dramatically were influenced by rearing systems. Breast muscle samples from birds reared under the conventional system had a smaller hue angle and saturation value than those from the free-range birds. Moreover, the drip loss parameter was significantly higher in free-range chickens. The ash and protein contents of breast muscles were similar although raw breast meat from free-range birds had significantly lower fat content. The results prove that a free-range rearing system can modify the appearance, color values, and fat content of chicken meat and it can be a part of the interests of meat production consumers.

Keywords: Broiler chickens, Free-range, Hubbard JA57, Intensive rearing system, Meat quality

INTRODUCTION

Chickens were primarily raised on family farms outdoor until around the 1950s (Alvarado et al., 2005). Since then the remarkable growth of chicken meat production commenced when the modern poultry industry began. This has led to developing intensive rearing systems, ensuring highest effectiveness and profitability of production (Bogosavljevi-Boskovic et al., 2012). However, intensive systems and rapid growth can cause animal stress, resulting in undesirable physiological and behavioral responses which lead to poor performance and meat quality (Xing et al., 2019) and occurrence of idiopathic myopathies, white striping, wooden breast, as well as pale, soft and exudative (PSE)-like meat (Ishamri and Seon-Tea, 2017). In contrast, free-range system can decrease stress conditions and allow better chicken welfare without causing any environmental confinement on broilers (Santos et al., 2005; da Silva et al., 2017). The poultry meat quality, in general, is an extremely complex concept that can be evaluated from different aspects because it is dependent on numerous factors, including genotype, sex, age, diet, density, environment and also rearing system (Berg, 2001; Brown et al., 2008; Miele, 2011; da Silva et al., 2017). In this respect, over the last decades, poultry meat production has paid particular attention to animal welfare, high-quality food safety standards, and different rearing systems. So, the competitiveness in this market has been radically changed into equally both price and quality competitiveness (Berg, 2001; Yeung and Morris, 2001; Bogosavljevic-Boskovic et al., 2010; Saleh et al., 2015).

From the prevailing viewpoint, broilers should have not only high slaughter yields and desirable carcass conformation scores, but also proper aesthetic, nutritional, and healthy characteristics. Hereupon, the chemical composition of chicken meat is another essential factor of broiler meat quality (Berg, 2001; Yeung and Morris, 2001; Castellini et al., 2008; Wang et al., 2009; Miele, 2011; Saleh et al., 2015; Srednicka-Tober et al., 2016). According to previous studies, broilers that had outdoor access showed better meat quality considering chemical

To cite this paper: Davoodi P and Ehsani A (2020). Characteristics of Carcass Traits and Meat Quality of Broiler Chickens Reared under Conventional and Free-range Systems. *J. World Poult. Res.*, 10 (4): 623-630. DOI: https://dx.doi.org/10.36380/jwpr.2020.71

composition and healthy characteristics of produced meat (Berg, 2001; Castellini et al., 2008; Miele, 2011; Saleh et al., 2015; Srednicka-Tober et al., 2016). Castellini et al. (2002) and Lin et al. (2014) also claimed that chemical contents in the chicken meat produced in free-range were better than those from other conventional systems, also meat sensory scores and overall acceptability in the free-range group were higher than those in other systems. In addition, high protein content, and low fat in meat of free-range chickens offers a healthier diet choice (Lin et al., 2014). Given that the consequence of rearing systems can differ by fattening length, the density of the flock, time to access free range, climatic factors, seasons and breeds, the results reported in previous studies are often quite variable (Bogosavljevi-Boskovic et al., 2012; Srednicka-Tober et al., 2016). Some authors have reported no significant effect of rearing system on carcass yields and meat quality traits but others have obtained statistically significant differences (Wang et al., 2009). Therefore, the objective of the current study was to evaluate the growth performance, carcass characteristics, and meat quality of Hubbard JA57 strain (known for free-range rearing) in both conventional and free-range systems in Iran condition.

MATERIALS AND METHODS

Ethics approval

The Ethics Committee on the Use of Animals of Tarbiat Modares University, Iran approved all the experiments and protocols used in this study (14-67626). All experimental protocols were applied in accordance with relevant legislation and recommendations by this committee.

Experimental schedule and sample collection

This trial was carried out at the Poultry Experimental Farm in Tarbiat Modares University, Iran from September to November 2017. The test material used in this study included a total of 82 fertile eggs of slow-growing Hubbard JA57 strain imported from Denmark. The eggs were placed in an incubator (Victoria Como, Italy) with the broad end pointing upwards and proper temperature and humidity. At the end of 18 days of incubation, the eggs were transferred into individual pedigree hatch bags sewn with a net fabric in order that chicks could be traced back to their initial egg weights. The hatch was pulled at day 21.5 with hatchability of 91%, then all 74 day-old chicks generated were identified with left leg tags using plastic cable ties and housed in a standard conventional system until the end of week 5 and then divided randomly into two groups each with 36 birds, one was reared in the same house and the other was transferred to the free-range system until the end of the rearing period of 11 weeks. Birds were provided with the same starter and finisher diets (Table 1), formulated based on the chemical composition of ingredients and broiler nutritional requirements according to NRC (NRC, 1994). The summary of the rearing systems conditions is given in Table 2. At the end of the rearing period of 11 weeks, 12 male broilers (6 from each rearing system) with a target weight range of 3.2 to 3.5 kg were randomly chosen to provide materials for analysis and sent to the chicken slaughterhouse related to the Department of Animal Sciences of Tarbiat Modares University, Iran to assess carcass characteristics and meat quality. After fasting for 12 hours before slaughter, all birds were weighed individually, slaughtered, and processed using standard commercial practices. All of them were used for physical, chemical, raw and cooked product analyses. The organ weights (liver, spleen, gizzard, heart, bursa of Fabricius) were recorded.

Table 1. Ingredients of starter and finisher diets and Dry matter based proximate chemical composition of diets.

Item	Starter (1-4 weeks)	Finisher (5-11 weeks)
Ingredient		
Maize	59.78	66.00
Soybean meal	28.52	22.00
Soybean oil	4.50	3.80
Wheat bran	4.56	5.92
Dicalcium phosphate	1.05	0.60
Limestone powder	0.90	1.05
Mineral and Vitamin Mix	0.34	0.34
Salt	0.10	0.10
Lysine	0.10	0.13
Methionine	0.15	0.06
Threonine	0.00	0.06
Chemical composition		
Metabolizable energy (kcal/kg)	3100	3150
Crude protein (%)	23.00	20.00
Crude fiber (%)	2.44	2.60
Ether extract (%)	7.16	6.20
Lysine (%)	1.12	1.00
Methionine (%)	0.50	0.39
Calcium (%)	1.00	0.90

Table 2. Summary of rearing conditions for chickens raised under two different systems.

Items	Conventional rearing system	Free-range rearing system
Outdoor access	No access	Access after week 5
Diet	*Ad libitum* regular diet with no animal ingredient	*Ad libitum* regular diet with no animal ingredient + access to pasture
Water	*Ad libitum*	*Ad libitum*
Vaccine program	Regular vaccination against Newcastle	Regular vaccination against Newcastle
Antibiotic	No antibiotic	No antibiotic
Slaughter age (day)	78	78

Measurements and evaluations

The meat quality variables, carcass component yield, initial and ultimate pH, color coordinates (Lightness, L*; redness, a*; yellowness, b*), Hue angle, saturation, drip loss, and water-holding capacity were measured. Also, cooked breast samples were evaluated for cooking yield (Mikulski et al., 2011).

Carcass component yield

The carcass weight was obtained after removing the head, neck, and shanks. Then, the main commercial segments (e.g., warm carcass, breast, and leg) and marginal parts (e.g., wings, abdominal fat, spleen, testicles, heart, and gallbladder) were weighed. Finally, the values were expressed as a percentage of carcass weight (Santos et al., 2005; Comert et al., 2016).

pH

The initial pH (45 min after slaughtering) and ultimate pH (pH in 24 h after slaughtering) were measured on raw homogenized breast muscles of six chickens from each group with three replications, in the same procedure. Approximately 2.5 g of meat was removed from the center of each pectoral major muscle, minced by mortar and pestle, and suspended in 25 mL distilled water then centrifuged for 5 min at 6000 rpm. Measurement of pH was performed using a digital pH meter equipped with a sensitive electrode, the device was calibrated before measurement at pH 4.0 and 7.0 buffer solutions (Choo et al., 2014).

Cooking loss

Cooking loss was determined by weighing meat before and after cooking. Meats were enveloped in an aluminum foil and cooked in an electric oven at 100 °C for 15 min, then samples were removed from the oven and left to cool at room temperature (Lin et al., 2014).

Drip loss

Drip loss was measured by keeping samples suspended in covered plastic bags on plastic racks for 48 h at 2 °C and calculated as a percentage of weight loss during storage (Funaro et al., 2014).

Water-holding capacity

Water-holding capacity was determined by the filter paper press method to obtain expressible meat juice. A 1000 mg raw meat sample was placed between several pieces of filter paper with 11 cm diameter and pressed for 5 min. Expressed juice of meat was defined as the loss in weight after pressing and expressed as a percentage of the initial weight of the raw meat sample (Wierbicki and Deatherage, 1958; Lee, 1995).

Color

The color profile of lightness, L*; redness, a*; yellowness, b* was measured by a reflectance colorimeter (ColorFlex EZ Spectrophotometer, USA) in triplicate on raw breast meat. The device was calibrated with black and white standards before meat color determination. Hue angle and saturation index were measured using formulas h_{ab} = arctan (b*/a*) and S = ([a^{*2} + b^{*2}]^{½})/ L*, respectively (da Silva et al., 2017).

Proximate analysis

Protein, fat, and ash content of raw breast were each independently measured with three replications from each of 6 broilers from free-range and 6 broilers from standard rearing system. Samples for proximate analysis were frozen until analyzed at the laboratory of the Animal Science Faculty of Tarbiat Modares University. Protein, fat, and ash content was measured following the AOAC methodology (Lee, 1995).

Statistical analysis

The R 4.0.2 software was used for statistical analysis. Pairwise treatment differences between carcass traits obtained from two different rearing system were determined with the Student t-test and any differences were considered significant at $p < 0.05$, for this reason, data were summarized as mean ± standard deviation and analyzed by one-way analysis of variance taking the rearing system as the main effect.

RESULTS

The comparison of carcass traits between the two rearing systems is reported in Table 3. There were no significant effects of rearing systems on the main carcass parameters measured. The results of physical and chemical meat characteristics comparison between conventional and the

free-range system are presented in Table 4. The initial pH of the breast meat from free-range broilers was slightly lower than conventional even though the ultimate pH of the breast meat became higher in free-range than conventional birds. These differences were not statistically significant but the difference of initial and ultimate pH values in free-range birds showed significant change ($p = 0.004$).

Table 3. Carcass characteristics of chickens reared under conventional and free-range systems.

Trait	Conventional system	Free-range system	t statistics	p-value
Live Weight (g)	3548.33	3371.67	-1.279	0.229
Carcass Weight (g)	2770.83	2560.00	-1.722	0.115
Drop Carcass (g)	777.50	811.67	0.758	0.465
Tight (%)	25.56	25.31	-0.424	0.680
Breast (%)	26.87	27.29	0.509	0.621
Wings (%)	11.63	10.97	-1.353	0.205
Legs (%)	4.57	4.74	1.197	0.258
Liver (%)	2.10	2.22	0.899	0.389
Abdominal fat (%)	2.50	2.53	0.114	0.911
Gizzard (%)	1.46	2.45	2.002	0.096
Testicle (%)	0.15	0.07	-2.314	0.061
Burse (%)	0.13	0.18	1.299	0.222
Gallbladder (%)	0.15	0.10	-1.908	0.085
Spleen (%)	0.19	0.22	1.360	0.203
Heart (%)	0.63	0.60	-1.244	0.241

Each group contained 36 chickens. *Statistically significant at $p < 0.05$

Table 4. Chicken carcass quality traits in conventional and free-range rearing systems.

Meat quality traits	Conventional system	Free-range system	t-statistics	p-value
pH measures				
Initial pH	5.81 ± 0.11	5.78 ± 0.15	-0.379	0.713
Ultimate pH	5.77 ± 0.14	5.83 ± 0.09	1.450	0.178
pH difference	-0.04 ± 0.10	0.05 ± 0.10	3.727	0.004*
Meat quality metrics				
Cooking loss	29.33 ± 2.45	28.10 ± 1.70	-1.259	0.237
Drip loss	3.24 ± 1.22	3.70 ± 1.60	2.384	0.038*
Water holding capacity	53.03 ± 2.32	55.26 ± 1.80	1.92	0.08
Color parameters				
Lightness	59.92 ± 0.33	52.00 ± 2.70	-7.008	0.000*
Redness	7.29 ± 1.79	3.40 ± 1.30	-4.309	0.002*
Yellowness	11.01 ± 2.04	13.20 ± 0.90	2.461	0.034*
Hue angle	56.40 ± 10.03	75.60 ± 4.80	4.233	0.002*
Saturation	13.40 ± 1.29	13.70 ± 1.00	4.902	0.001*

Data are expressed as mean ± standard deviation. Each group contained six chickens. *Statistically significant at $p < 0.05$.

Table 5. Proximate analysis of raw breast meat from conventional and free-range broilers.

Proximate analysis	Conventional system	Free-range system	t-statistics	p-value
Protein, %	23.85 ± 0.41	24.20 ± 0.54	1.23	0.24
Fat, %	4.01 ± 0.40	3.18 ± 0.40	-3.57	0.005*
Ash, %	3.03 ± 0.21	3.05 ± 0.28	-0.12	0.90

Data are expressed as mean ± standard deviation. Each group contained six chickens. *Statistically significant at $p < 0.05$

The effect of the two rearing systems on meat quality did not represent a significant difference in terms of the cooking loss and water holding capacity parameters, however, the drip loss parameter was affected by rearing systems significantly ($p = 0.038$). All the color coordinates L*, a*, b*, hue angle, and saturation value also showed extremely significant differences between the rearing systems. Breast muscle from free-range birds revealed significantly lower L* and a* values making it paler in comparison to conventional breast muscle. The smallest difference was seen in the b* coordinate with the breast muscle from the free-range birds which was significantly higher than conventionally reared birds, so breast meat in free-range was more yellow ($p = 0.03$) than conventional.

The result of the proximate analysis of the raw breast meat produced from chickens reared under conventional and the free-range system is reported in Table 5. Raw breast meat from free-range birds had significantly ($p = 0.005$) lower fat content in comparison to broilers reared conventional system, however, no significant differences ($p > 0.05$) was observed for protein and ash content of the raw breast meat.

DISCUSSION

A growing knowledge of human health, food safety, and animal welfare interests have led to the great transformation in animal rearing systems and particularly free-range product markets all over the world. Chicken meat produced in alternative systems, such as free-range or organic, are part of this orientation. It is specified that slaughtering age, genetic breeds (fast and slow-growing), physical activity, and pasture intake are key factors in chicken meat quality.

In this research, no significant differences were observed in yield of carcass parts. The result has no consistency with the findings of Mikulski et al. (2011) who reported the significant influence of rearing system on carcass yields. Several studies also reported that body weight, body weight gain, and the proportion of breast meat of birds from the free-range system were significantly lower than of those reared in indoor floor system (Grashorn and Serini, 2006; Dou et al., 2009; Wang et al., 2009). Conversely, some other researchers have found that free-range chickens had the higher live weight, breast, and thigh-drumstick weights compared to the conventional system (Alvarado et al., 2005; Santos et al., 2005; Połtowicz and Doktor, 2011; Lin et al., 2014; Comert et al., 2016) and also there are some other results reported by different researchers that were consistent with findings of the current study as they claimed that most of the carcass yield, especially body weight, did not show significant changes (Cheng et al., 2008; Chen et al., 2013; Fu et al., 2015).

The meat quality attributes including color values, pH measures, and water holding capacity were evaluated in this experiment because these parameters can have important effects on the characteristics of fresh chicken meat at the point of sale (Kim et al., 2020).

In the present study, the initial and ultimate pH of breast meat were slightly affected by two rearing systems but the changes were not significant and this finding was consistent with the results of many studies (Cheng et al., 2008; Husak et al., 2008; Ponte et al., 2008; Wang et al., 2009; Mikulski et al., 2011; Li et al., 2017). Although the initial and ultimate pH values were not significantly different between the two rearing systems, their variation obviously showed a different pattern that could be deduced why some studies have concluded that meat from broilers reared in the free-range system had lower shelf-life stability compared with conventionally reared broiler meat (Alvarado et al., 2005; Husak et al., 2008; Funaro et al., 2014). Because pH, microorganism content, and oxidation are intra-dependent factors and pH alteration during storage can be resulted by proteolytic degradation or fat oxidation which is decreases shelf-life of meat (Kim et al., 2020). This notable different pattern in pH change in breast meat of free-range birds might be the result of intensive physical activity and more pre-slaughter stress in comparison to the conventional broilers (da Silva et al., 2017; Kim et al., 2020). Pre-slaughter stress and physical activity in free-range chicken may lead to the range of

chemical changes based on the conversion of ATP to ADP and also anaerobic glycolysis of glycogen storage in muscles decreases pH due to lactic and pyruvic acid production so finally it can change the meat acidity during the rigor mortis.

The influence of the two studied rearing systems on meat quality did not reveal a significant difference in the cooking loss and water holding capacity parameters, although, drip loss parameter was affected by rearing systems significantly. The result of water holding capacity concurs with similar studies in comparing breeding methods (Castellini et al., 2002; Cheng et al., 2008; Dou et al., 2009; Wang et al., 2009; Stadig et al., 2016; Li et al., 2017). Water holding capacity is an important attribute of meat quality, if water holding capacity is poor, meat and meat products will lack juiciness. As slow-growing chickens are better suited to the free-range system (Castellini et al., 2008; Kingori et al., 2010; Bogosavljevi-Boskovic et al., 2012), but Fanatico et al. (2007) claimed that slow-growing birds had weaker water-holding capacity but their meat is more tender than the fast-growing birds.

The absence of significant differences in the carcass yield and other studied traits between two different systems are may be due to short rearing period with outdoor access. An experiment was conducted to evaluate the effect of free-range days on growth performance, carcass yield, and meat quality; and it was reported that increasing free-range length advantageously affects breast yield, but decreases thigh, and foot yields as well as the water-holding capacity of the thigh. No evidence was found that free-range days can change growth performance and meat quality (except water holding capacity) (Tong et al., 2014).

It can be demonstrated that free-range rearing system can modify the color values in chicken meat as the findings showed the breast meat from free-range broilers had higher yellow color and much lower red color than another rearing system (Brown et al., 2008; Połtowicz and Doktor, 2011; Funaro et al., 2014; da Silva et al., 2017). Of course, it should not be ignored that there were some peculiarities in results reported by authors about meat color values in comparing two standard and free-range meat yield.

According to the present result, raw breast meat from free-range birds had significantly lower fat content in comparison to conventional broilers, which could be important to consumers concerned with fat intake. The obtained results in previous studies suggested that the free-range rearing system was more favorable than the conventional system, as it resulted in significantly higher protein content and a lower fat content of chicken meat (Bogosavljevi-Boskovic et al., 2012) however, no significant differences were observed for protein and ash content of the raw breast in the present study.

CONCLUSION

Although the quantitative carcass traits showed less significant differences between the two groups, some main qualitative traits including apparent characteristics such as all color coordinates and drip loss were significantly affected by the free-range system. Moreover, fat percentage of raw breast meat was significantly lower in the free-range production system, therefore, it could be healthier. Accordingly, no significant differences in the amount of meat produced in two rearing systems showed that the conventional production system in the poultry industry can be successfully replaced by alternative systems such as free-range without production loss. Also, the different chemical composition of meat in the free-range system may become more attractive in terms of increasing healthy food demand in the world industry. Ultimately, further studies are suggested to investigate consumer preferences, especially in terms of sensory evaluation of meat from the two production systems.

DECLARATIONS

Competing interests

We certify that there is no conflict of interest with any financial organization regarding the aspects discussed in the manuscript.

Authors' contributions

Alireza Ehsani designed the experiments, guided the research team, and edited the final draft of the manuscript. Peymaneh Davoodi performed field and lab researches, analyzed the data, and wrote the paper. Finally, all authors read and approved the final manuscript.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 631-642, December 25, 2020

Research Paper, PII: S2322455X2000072-10

DOI: https://dx.doi.org/10.36380/jwpr.2020.72

Effect of *Amphora coffeaeformis* and *Star anise* as Dietary Supplementson the Immunity and Growth Performance of Broiler Chickens

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Received: 07 Nov. 2020
Accepted: 20 Dec. 2020

ABSTRACT

The present study was designed to evaluate the impacts of daily dietssupplemented with *Amphora coffeaformis* and *Star anise* on growth performance and immunity of Cobb broiler chickens. *Amphora coffeaformis* is considered a potent free radical scavenger due to the presence of β-carotene and fucoxanthin, which are used widely as food additives. *Star Anise* has a natural antioxidant, which can also be used for the chemo-prevention of disease occurring due to oxidative deterioration. A total of 270 broiler chickens were divided into three groups, each with three replicates of 30 birds. The control group (G1) was given the basal diet, the *Amphora* group (G2) received *Amphora* in a dose of 1g/Kg in the ration, and the *Star anise* group (G3) received *Star anise* in a dose of 2g/Kg in the ration. The results indicated that *Amphora* and *Star anise* significantly improved the final body weight, weight gain, and feed conversion ratio, total white blood cells count, phagocytic activity percentage, phagocytosis index in plasma, IgM, IgG, and A/G ratio in serum. In addition, *Amphora* and *Star anise* significantly increased mRNA expression of hepatic growth hormone gene, insulin-like growth factor-1 (IGF-1) genes (IGF1), and mRNA expression of splenic interferon-gamma (INF-γ) and Interleukin 12 (IL-12p35) genes from broiler chickens, compared to the control group. In conclusion, the use of fed additives, such as *Amphora coffeaeformis*and *Star anise* in the diet of broiler chickens for 35 days was sufficient to improve broiler growth performance and could modulate their immunity.

Keywords: *Amorpha coffeaeformis*, Broiler chickens, Diet supplementation, Growth performance, Immunity, *Star anise*

INTRODUCTION

Global food production is facing a greater challenge than ever before. Protein in particular is one of the most important nutrients in animal and human life (FAO, 2018).

Broiler production as a source of protein has become an important issue in many growing countries. However, the recent increase in the costs of traditional feed was once a major contributor to net returns from the poultry business. Feed accounted for 70-80 percent of the total costs of poultry production (Bolu and Balogun, 2004). It was found that reducing feed costs using cheaper and more unconventional feed was once a required problem for commercial poultry production (Bhatta and Sharma, 2001). The feed additives are a collection of nutrients and non-nutrients compounds that help to increase the competence of feed usage and thus reduce the high feed costs. In recent years, these additives have played an important role as feed supplements for many purposes in poultry production (Zhang et al., 2009).

Microalgae were identified as microscopic, unicellular, and photosynthetic organisms and can grow in saline and freshwater which provide a rich supply of nutrients and biologically active compounds, such as proteins, amino acids, polyunsaturated fatty acids, microelements, vitamins, antioxidants called carotenoids, which have long records of human application as a food (Belotti et al., 2014). Microalgae of exclusive species could be properly involved in poultry diets, which can affect advisably on birds' health, performance, and comfort of chickens' meat and egg (Abdelnour et al., 2019).

Microalgae were considered to be an adequate supply of a large number of metabolites that were suitable for animal feed. These metabolites included proteins,

carbohydrates, fats, vitamins, and minerals (Andrade et al., 2018).

Currently, microalgae are receiving more attention in the market as nutraceuticals and fitness meals. Several microalgae, such as Spirulina, Chlorella, and *Amphora* are grown commercially for the production of algal products such as β-carotene, lutein, and phycocyanin (Hirata et al., 2000). *Amphora* is a major genus of diatoms of marine and freshwater origin (Parnell and Trevor, 2007).

*Amphora coffeaformi*s is one of the most common alkaline fresh ecosystems and brackish-water localities (Bhosleac et al., 1993). *Amphoracoffeaformis* has strong antioxidant activity against lipid peroxidation (Sugiharto et al., 2018), and is rich in polyunsaturated fatty acids (PUFAs), especially Docosahexaenoic (DHA), Eicosapentaenoic (EPA), and α-linolenic acid (Lee et al., 2009).

The microalga was a source of bioactive compounds including *Amphora coffeaeformis*, especially the carotenoids, sulfated polysaccharides, polyunsaturated fatty acids, α-tocopherol, especially β-glucans, in addition to vitamins C and E (El-Sayed et al., 2018)

Several studies on diatoms such as Amphora showed the possibility of their extract to use in both protective and antioxidant agents (Mekkawy et al., 2020), except for their antibacterial (Ayoub et al., 2019), antiviral (Abdel-Wahab, 2018), anti-inflammatory factors (Lauritano et al., 2016) and their dietary supplements (Selvaraj et al., 2013).

Amphora coffeaeformis was considered as a potent radical scavenger due to the presence of β-carotene and fucoxanthin, which are widely used as food additives in addition to the various nutraceutical applications such as pro-vitamin (Jaswir et al., 2011). The oral administration of *Amphora coffeaeformis* at three attentions (10, 20, and 30g / kg diet) in Nile tilapia (*O. niloticus*) diets led to enhance in growth performance, feed efficiency, and serum lysozyme (Ayoub et al., 2019).

Herbs are mixed into poultry diets to replace synthetic products and to stimulate or promote the efficient use of feed nutrients, which may subsequently result in faster body weight gain, higher production rates, and increased feed efficiency. In addition, active ingredients in herbs could improve digestion and stimulate the immune functions of broilers (Ghazalah and Ali, 2008; Shawky et al., 2020 a, b).

Star anise is a medium-sized evergreen tree that is native to southwest China and is also extensively cultivated in the subtropical and tropical regions of Asia (Benmalek et al., 2013; Elmasry et al., 2018). It has been shown that *star anise* promoted digestion, and has antioxidant, antibacterial, antiparasitic, antipyretic, and antifungal properties (Ertas et al., 2005; Mohammed, 2008).

However, anethole is an important compound in the *Star anise*, the other important compounds in the seeds include p-anisaldehyde, anise alcohol, acetophenone, pinene, and limonene. Seeds have excellent supplies of minerals such as calcium, iron, manganese, magnesium, zinc, potassium, and copper. This essential spice contains precise amounts of antioxidant nutritional vitamins such as vitamin C and vitamin A (Zhou et al., 2005). Shikimic acid, which is a component in *Star anise*, is one of the best components of the antiviral drug Tamiflu for combating avian influenza (Ohira et al., 2009; Borah, 2015). *Star anise is* pronounced to possess antioxidant residences (Chempakam and Balaji, 2008) as well as a tremendous anticancer (Shu et al., 2010).

MATERIALS AND METHODS

Ethical approval

The experimental design was approved by the Ethical Research Committee of the Faculty of Veterinary Medicine, the University of Sadat City, Egypt with approval number VUSC-014-2-18.

Experimental animals

The current study was conducted in the Department of Physiology, the University of Sadat City, Faculty of Veterinary Medicine, Sadat City, Egypt, on 270 Cobb broiler chickens that were one-day-old and had an average weight of 45.0 ±2.0 gram (Cobb strain) of the Misr-El-Arabia Company for Poultry.

Feed and water were supplied *ad libitum*, and synthetic lights were supplied 24 hours a day for the first 15 days to assist newly hatched chickens to commence drinking and eating. After two weeks, one hour of darkness was applied once a day. The chickens were reared at 33°C to 34°C for the first week, and then regularly decreased by 2-3°C per week until the temperature reached around 21 to 23°C, while the relative humidity was maintained around 55 to 65 percent. Chickens were reared in the poultry house, equipped with feeders, drinkers, and wood shaves used as bedding material. Strict sanitation practices were applied during some stages of the experiment. The chickens were reared under comparable environmental conditions. The experimental house was warm, dry, and free from drafts. Sparkling air provided some sort of ventilation to remove excess moisture and ammonia from the facility.

Nutrition

Chickens were feed starter rations that contained all of the necessary nutrients needed for maintenance, growth, and reproduction from day one to day 14. At the beginning of the third-week, chickens fed on the finisher ration (Table 1).

Table 1. The ingredients and chemical analysis of basal diet of broiler chickens

Ingredients and composition (%)	Starter	Finisher
Corn	55.59	61.07
Soybean meal	37.32	31.83
Soy oil	2.98	3.41
Lime stone	1.21	1.42
Dicalcium Phosphate	1.60	1.16
DL. Methionine	0.20	0.10
*Vitamin and Minerals	0.60	0.60
Sodium chloride	0.23	0.18
Sodium bicarbonate	0.27	0.23
Chemical Analysis (%)		
Metabolizable energy(ME) kcal/kg	2950	3050
Crude Protein (%)	21.20	19.16
Lysine (%)	1.14	1.01
Methionine (%)	0.50	0.39
Methionine and Cysteine (%)	1.03	0.84
Available Methionine + Cysteine (%)	0.85	0.71
Calcium (%)	0.93	0.90
Available Phosphate (%)	0.44	0.35

*Supplied per kilogram of diet: vitamin A, 1,500 IU; cholecalciferol, 200 IU; vitamin E, 10 IU; riboflavin, 3.5 mg; pantothenic acid10 mg; niacin, 30 mg; cobalamin, 10 µg; choline chloride, 1,000 mg; biotin, 0.15 mg; folic acid, 0.5 mg; thiamine 1.5 mg; pyridoxine 3.0 mg; iron, 80 mg; zinc, 40 mg; manganese, 60 mg; iodine, 0.18 mg; copper, 8 mg; selenium, 0.15 mg.

Preparation of *Amphora coffeaeformis* extract

Amphoracoffeaeformis extract was obtained from the Algae Production Unit (APU), National Research Institute (center), Cairo, Egypt. The extract was previously identified for its phytochemical constitute using liquid chromatography-mass spectrometry (Mekkawy et al., 2020).

Preparation of *Star anise*

The dried *Star anise* was purchased from a local market and was added to the diet after grinding into powder.

Animal grouping

From the seventh day of the experiment, the chickens were divided into three groups with three replicates of 30 birds each. The chickens were raised on the floor with given water and diet *ad libitum*. All chickens were vaccinated against Newcastle Disease (ND) and Infectious Bronchitis (IB) strains HIB120 at ninth days of age and against infectious bursal disease (Gumboro) at the 13thday of age. From day 16 to 35, no vaccination was given against any disease. Chickens were randomly divided into three experimental groups, including group 1 (control group), which chickens only received basic ration; group 2, which ration was mixed with *Amphora* at a dose of 1g / kg feed (Mekkawy et al., 2020), and group 3, in which the chickens received a ration mixed with *Star anise* at a dose of 2 g /kg feed (Alhajj et al., 2015; Ding et al., 2017).

Growth performance parameters

The growth performance parameters of broiler chickens have consisted of Body Weight (BW, gram), Body Weight Gain (BWG), Feed Intake (FI), and Feed Conversion Ratio (FCR). All chickens in groups had been weighed individually at the start and the end of the experiment. The body weight gain of chickens (expressed in grams) in each group was calculated by the difference between 2 successive weights (Nwanna, 2003).

Weight gain = (W2- W1)

Where W1 is the mean chicken weight at the beginning of the experiment and W2 is the mean chicken weight at the end of the experiment**.**

The experimental diets were offered regularly to each group. The feeds offered were measured daily, and at the end of the week, the weekly feed consumption was determined by the difference between the weight of feed offered and remained part. The FCR was calculated by dividing the amount of FI (g) during the entire experimental period by the total BWG (g) as outlined by Abd El-Wahed (1998).

FCR = total FI (g) of chicken / total BWG (g) of chicken.

Sample collection

On day 35, blood samples were taken from the wing vein of 10 chickens per group with anticoagulant (EDTA) to obtain plasma. The plasma was separated from the blood cells by centrifugation at 3.000 rounds per minute (rpm) for 30 minutes to determine haematological and biochemical parameters. Thereafter, chickens were slaughtered, and then the liver, and spleen were removed

to estimate the mRNA expression of GH, IGF-1, IFN-γ, IL - 12p35 according to Cinthia et al. (2013).

Determination of haematological parameters

Red Blood Cells (RBCs), White Blood Cells (WBCs), Haemoglobin (Hb) concentration, and Packed Cell Volume (PCV) were estimated using automated technical analyserDirui Bcc-3600. The Mean Corpuscular Volume (MCV), Mean Corpuscular Haemoglobin (MCH), and Mean Corpuscular Haemoglobin Concentration (MCHC) were determined according to the method describing by Feldman et al. (2000). Differential leukocyte counts (heterophils, eosinophils, basophils, lymphocytes, and monocytes) were counted on blood smears stained with May-Grunwald-Giemsa (Tavares-Dias and Moraes, 2003). Phagocytosis of polymorph nuclear cells using *Candida Albicans* was performed in accordance with the method described by Sornplang et al. (2015).

Phagocytic Activity % = (Number of Heterophils ingesting candida ×100)/ Total number of Heterophils.

Phagocytic index = The total number of ingested candida / Number of active Heterophils.

Determination of biochemical parameters

The assay of total plasma proteins (g/dl) and albumin (g/dl) was carried out by a colorimetric method using commercial Diamond diagnostics kits according to the method described by Cannon et al. (1974) and Doumas et al. (1971), respectively.Serum alanine aminotransferase (ALT) and serum aspartate aminotransferase (AST) enzymes were determined colorimetrically using commercial kits of Bio diagnostics according to Reitman and Frankel, (1957). Creatinine (mg/dl) was determined by the colorimetric method using commercial kits of Biomed diagnostics according to Young (2001).Urea (mg/dl) was measured by the colorimetric method using commercial kits of Diamond diagnostics according to the method of Chaney et al. (1962). Protein electrophoresis profile was carried out by a Polyacrylamide Gel Electrophoresis according to Lewis et al. (2006).

Gene expression

Analysis of the mRNA expression of genes of Hepatic Growth Hormone and Insulin-like Growth Factor-1

The analysis of the mRNA of the expression of Growth Hormone (GH) and Insulin Growth Factor-1 (IGF-1) was performed at the Central Laboratory of the Faculty of Veterinary Medicine, Benha University, in Egypt. Liver samples were dissected from each group and then immediately frozen at -80°C. Total RNA was extracted from the frozen liver using the RNeasy® Mini kit (Qiagen) according to the manufacturer's protocol. The quantity and quality of RNA were determined using SPECTROstar Nanodrop. Single-stranded cDNA was synthesized from 1000 ng of total RNA according to the manufacturer's protocol for High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). The cycling conditions were 10 minutes at 25°C, 120 minutes at 37°C, and 5 minutes at 85°C. Total RNA and cDNA samples were then stored at -80° C until used. Expression of hepatic GH and IGF-1 genes was analyzed by real time-PCR using sense and antisense primers as previously described (Gasparino et al., 2014) by using the primers sets including GH sense (5 -′AAGGGATCCAAGCTCCTGAT-3′), and antisense (5 -′ATAACCACGTCCCTCAGTGC-3′); IGF-1 sense (5 -′ CACCTAAATCTGCACGCT-3′), and antisense (5 -′ CTTGTGGATGGCATGATCT-3′); and βactin as a housekeeping gene, sense (5ACCCCAAAGCCAACAGA-3′) and anti-sense (5 -′ CCAGAGTCCATCACAATACC-3′). PCR reactions for each gene were performed for each sample analyzed. Each PCR reaction consisted of 1.5 µ l of 1µg/µ l cDNA, 10 µ l SYBR Green PCR Master Mix (QuantiTect SYBR Green PCR Kit, Qiagen), and one µMof each forward and reverse primer for GH and IGF-1 genes while one µM forward and 1.5 µM reverse primer for βactingene and nuclease-free water to a final volume of 20 µl. The reactions were then analyzed on an Applied Biosystems 7500 Fast Real-time PCR Detection system under the conditions of 95°C for ten minutes (holding stage) and 40 cycles of 95°C for 15 seconds (denaturation stage) followed by 60°C for one minute (annealing and extension stage). Changes in gene expression were calculated from the obtained Cycle threshold (Ct) values, which were provided by real-time PCR instrumentation using the comparative Threshold cycle (TC) method for a reference (housekeeping) gene (βactin) (Gasparino et al., 2014).

Analysis of mRNA expression of splenic interferon-gamma and Interleukin 12 genes

Spleen samples were dissected from all groups and then immediately frozen at -80°C. Total RNA was extracted from the frozen spleen using the RNeasy® Mini kit (Qiagen) according to the manufacturer's protocol. The quantity and quality of the RNA were determined by using Spectrostar nanodrop Single-stranded cDNA was synthesized from 1000 ng of total RNA according to the manufacturer's protocol for High Capacity cDNA Reverse

Transcription Kits (Applied Biosystems). Cycling conditions were 25°C for 10 minutes, 37°C for 120 minutes, and 85° C for 5 minutes. Afterward, total RNA and cDNA samples were stored at -80° C until use. Each PCR reaction consisted of 1.5 µl of one µg/µl cDNA, tenµl SYBR Green PCR Master Mix (QuantiTect SYBR Green PCR Kit, Qiagen), one µM of each forward and reverse primer for INF-γ and IL-12p35 genes while one µM of forward and 1.5 µM reverse primer for βactin gene and nuclease-free water to a final volume of 20 µl. The Reactions were then analyzed on the Applied Biosystem 7500 Fast Real-time PCR Detection system under the conditions of 95°C for ten minutes (holding stage) and 40 cycles of 95°C for 15 seconds (denaturation stage) followed by 60°C for one minute (annealing and extension stage). Changes in gene expression were calculated from the obtained Cycle threshold (Ct) values provided by real-time PCR instrumentation using the comparative CT method for a reference (housekeeping) gene (βactin) (Gasparino et al., 2014).

Statistical analysis

The results were expressed as Mean ± Standard Error (SE). The relations between means in different groups were tested using a one-way analysis of variance (ANOVA). Duncan test was used for finding the significant differences in SPSS, 16 version. The P-values at 0.05 or lesser were considered significant.

RESULTS

The data in table 2 presented that the *Amphora* and *Star anise* supplementation resulted in a significant increase ($p < 0.05$) in the final BW, BWG, and also a significant decrease in the FCR compared to the control group ($p < 0.05$). The data in table 3 indicated that the Amphora and Star anise supplement did not significantly affect the erythrogram. The data in table 4 revealed that the *Amphora* and *Star anise* supplementation resulted in a significant increase ($p <0.05$) in total WBCs count, percentage of heterophils, H/L ratio, globulins (alpha 1 globulin, alpha 2 globulin, beta globulin, and gamma globulin), IgG, IgM, phagocytic activity, phagocytic index, while the total protein and albumin, lymphocyte percentage, and platelets count were not significantly affected. The data in table 5 revealed that the *Amphora* and *Star anise* supplementation did not significantly affect urea, creatinine, AST, and ALT ($p > 0.05$). The data in table 6 revealed that the *Amphora* and *Star anise* supplementation significantly increasedthe expression of hepatic GH and IGF1, and increased splenic INF-Gamma and interleukin12p35 compared to the control group ($p>0.05$).

Table 2. Effect of *Amphora* and *Star anise* supplementation on growth performances of broiler

Groups	Control group	*Amphora* group	*Star anise* group
Initial body weight (g)	192.83 ± 1.37a	195.08 ± 1.23a	194.01 ± 1.30a
Final body weight (g)	2054.9 ± 6.74c	2529.3 ± 10.20a	2297.8 ± 10.59b
Weight gain (g)	1824.60 ± 11.79^{c}	2349.90 ± 12.67^{a}	2195.90 ± 17.55^{b}
FCR	2.43 ± 0.03^{a}	1.62 ± 0.01^{c}	1.82 ± 0.02^{b}

In the same row, Mean ± Standard Error with different letters superscripts are significantly different at $P < 0.05$. FCR: Feed Conversion Rate.

Table 3. Effect of *Amphora* and *Star anise* supplementation on erythrogram of broiler

Groups	Control group	*Amphora* group	*Star anise* group
RBCs count ($10^6/mm^3$)	2.45 ± 0.08^{a}	2.60 ± 0.06^{a}	2.59 ± 0.07^{a}
PCV %	29.06 ± 0.61^{b}	30.94 ± 0.49^{a}	29.59 ± 0.62^{ab}
Hb (g/dl)	11.29 ± 0.20^{a}	11.68 ± 0.21^{a}	11.61 ± 0.17^{a}
MCV (μ^3)	111.50 ± 1.94^{a}	116.29 ± 1.62^{a}	116.40 ± 1.82^{a}
MCH (Pg)	38.94 ± 0.62^{a}	38.04 ± 0.85^{a}	37.86 ± 0.70^{a}
MCHC %	30.73 ± 0.27^{a}	31.45 ± 0.30^{a}	30.64 ± 0.39^{a}

In the same row, Mean±Standard Error with different letters superscripts are significantly different at $p<0.05$. RBCs: Red Blood Cells; PCV: Packed Cell Volume; MCV: Mean Corpuscular Volume; MCH: Mean corpuscular hemoglobin; MCHC: Mean Corpuscular Hemoglobin Concentration.

Table 4. Effect of *Amphora* and *Star anise* supplementation on immunity profile of broiler chicken

Groups	Control group	*Amphora* group	*Star anise* group
WBCs count (10^3/mm^3)	20.55 ± 0.17^c	32.99 ± 0.41^a	29.03 ± 0.42^b
Lymphocytes (%)	68.65 ± 0.74^a	67.80 ± 0.31^a	67.63 ± 0.32^a
Heterophils (%)	17.62 ± 0.34^c	27.01 ± 0.19^a	23.73 ± 0.32^b
H/L ratio	0.40 ± 0.003^a	0.35 ± 0.006^b	0.30 ± 0.007^c
Platelets count (10^3/mm^3)	310.25 ± 11.51^a	298.25 ± 9.20^a	310.85 ± 8.01^a
Total plasma protein (g/dl)	3.32 ± 0.03^a	3.47 ± 0.07^a	3.41 ± 0.06^a
Albumin (g/dl)	1.83 ± 0.03^a	1.67 ± 0.06^a	1.72 ± 0.06^a
Globulin (g/dl)	1.50 ± 0.02^c	1.80 ± 0.02^a	1.68 ± 0.02^b
Alpha 1 globulin (g/dl)	0.24 ± 0.003^c	0.34 ± 0.006^a	0.32 ± 0.008^b
Alpha 2 globulin (g/dl)	0.32 ± 0.004^a	0.32 ± 0.004^a	0.33 ± 0.005^a
Beta globulin (g/dl)	0.42 ± 0.004^c	0.48 ± 0.010^a	0.45 ± 0.004^b
Gamma globulin (g/dl)	0.51 ± 0.016^c	0.66 ± 0.009^a	0.60 ± 0.018^b
IgM (mg/dl)	50.02 ±.0.8^c	90.02 ± 0.5^a	80.47 ± 1.4^b
IgG(mg/dl)	20.95 ± 0.7^c	40.37 ± 0.5^a	40.14 ± 0.4^b
A/G ratio	1.22 ± 0.03^a	0.93 ±0.04^b	1.03 ± 0.04^b
Phagocytic activity (%)	49.79 ± 0.72^c	67.73 ± 0.73^a	63.69 ± 0.46^b
Phagocytic index	1.93 ± 0.050^c	2.83 ± 0.040^a	2.67 ± 0.026^b

In the same row, Mean ±Standard Error with different letters superscripts are significantly different at $p < 0.05$.WBCs: White Blood Cells; IgM: Immunoglobuline M; IgG: Immunoglobuline G; A/G ratio: albumin / globulin ratio; H/L ratio: Heterophils/ Lymphocytes ratio.

Table 5. Effect of *Amphora* and *Star anise* supplementation on liver function tests and kidney function tests of broiler

Groups	Control group	*Amphora* group	*Star anise* group
ALT (U/L)	191.60 ± 4.35^a	183.30 ± 3.67^a	187.60 ± 2.97^a
AST(U/L)	36.60 ± 1.21^a	33.90 ± 1.10^a	33.30 ± 1.15^a
Urea (mg/dl)	9.29 ± 0.10^a	8.91 ± 0.13^a	9.35 ± 0.13^a
Creatinine(mg/dl)	0.45 ± 0.010^a	0.42 ± 0.005^a	0.44 ± 0.006^a

In the same row, Mean ± Standard Error with different letters superscripts are significantly different at $p < 0.05$.ALT: Serum alanine aminotransferase; AST: serum aspartate aminotransferase.

Table 6. Effect of *Amphora* and *Star anise*supplementation on mRNA expression of growth hormone, Insulin-like growth factor1, Interferon gamma, Interleukin12p35 of broiler chicken, data represented as fold change among different experimental groups

Groups	Control group	*Amphora* group	*Star anise* group
GH	1.27 ± 0.11^b	9.11 ± 0.13^a	8.25 ± 0.21^a
IGF1	1.05 ± 0.03^b	3.78 ± 0.08^a	2.73 ± 0.08^a
INF gamma	1.25 ± 0.03^b	7.60 ± 0.15^a	6.36 ± 0.06^a
IL - 12p35	0.90 ± 0.04^b	2.14 ± 0.06^a	1.81 ± 0.05^a

In the same row, mean ± Standard Error with different letters superscripts are significantly different at $P < 0.05$. GH: hepatic growth hormone; IGF-1: insulin-like growth factor-1; INF-γ: splenic interferon-gamma; IL-12p35: Interleukin12p35.

DISCUSSION

Poultry meat is the second largest food product in the world (Manning et al., 2007). In order to endure poultry production the meet global demand, antibiotic replacements were required (Mcdevitt et al., 2006). In the present study, chickens that were fed a diet supplemented with *Amphora coffeaeformis* and *Star Anise* significantly enhanced their growth performance compared to the control group. This result is attributed to the fact that *Amphora coffeaeformis* significantly improved appetite, which led to higher FI and improved growth (Ayoub et al.,

2019). These results were compatible with those reported by Zhao et al. (2004), who concluded that *Amphora*-treated chickens indicated an increased average daily gain and an improvement in the FCR due to the improvement in the digestibility of nutrients.

The improvement in the FCR could also be due to the fact that *Amphora coffeaeformis* contained several nutrients, especially vitamins and minerals that could aid in promoting growth (Belay et al., 1996). The positive effects of *Amphora* could be due to its bioactive compounds, which have antioxidant, anti-inflammatory, antiviral, and antibacterial effects (Rajput and Mishra, 2012; Salahuddin et al., 2017).

Star anise had a positive effect on the live BW, BWG, and FCR of broiler chickens (Al-hajj et al., 2015). The improvement in broiler performance could be due to the active component in *Star anise*, anethole, which could lead to better digestion by inducing the secretion of endogenous enzymes, better absorption, and improved microbial balance in the gut. Amad et al. (2011) stated that the inclusion of essential oils from thyme and *Star anise* resulted in an improvement of the digestibility of the crude protein, crude ash, crude fat, calcium, and phosphorus. This enhancement in the digestibility also led to an increased surface area for absorption in the intestine and improved nutrient absorption. Additionally, it was found that essential oils had a stimulatory effect on pancreatic enzymes (Rao et al., 2003).

The present study revealed no significant difference in blood parameters between the treatment groups the control group. The present results were in agreement with Soltan et al. (2008) and Mekkawy et al. (2020), who reported that there were no significant differences in blood profiles in groups that supplemented with *Star anise* seed and *Amphora*.

In the present study, the addition of *Amphora* and *Star anise* improved the immunity indices in broilers such as phagocytic activity, gamma globulins, IgM, and IgG. *Amphora coffeaeformis*activated the immune system of the chickens and became resistant to pathogenic bacteria, which was consistent with the finding of Mariey et al. (2012) and Jamil et al. (2015). This activation of the immune system could be due to *Amphora*, which was rich in different pigments and polyphenolic compounds, catechin, gallic acid, and p-coumaric acid (El-Sayed et al., 2018). Also, Jaswir et al. (2011) revealed that *Amphora coffeaeformis* was known to be a potent radical scavenger due to the presence of β-carotene and fucoxanthin, which were often used as food additives in addition to the various nutraceutical applications such as pro-vitamin A, antioxidant, anticancer, and anti-obesity.

Feeding chickens with *Star anise* resulted in a significant increase in the immunity indices of all groups. It might be due to the fact that *Star anise* modulates the immune system by stimulating various immune cells such as macrophages, monocytes, Natural Killer Cell (NKC) and effects on cytokines/chemokines in various *in vitro* and *in vivo* trials (Shahrajabian et al., 2019; Sung et al., 2012 a, b).

The results of *Amohora* which activated the immune system agreed with Kang et al. (2013), who found a significant increase in the lymphocyte counts in algae-fed broilers compared to other chickens. The phagocytic activity was also significantly increased in treated animals that were fed with algae and improved the immune response (An et al., 2010). Also, Khan et al. (2012) reported that the immunomodulatory effects of natural feed additives were linked to their ability to increase phagocytosis of potential macrophages, the production of interleukins, interferon-Y, and tumor necrosis factor, increase the secretory metabolism of macrophages, antigen-presenting cells, and antioxidant functions.

The present findings were in accordance with Abdelnour et al. (2019), who noted that IgG and IgM levels were increased in broilers that consumed food containing algae. Immunoglobulins increasing could be because several types of unicellular microalgae are excellent sources of immunoregulatory polysaccharides, such as β-glucan, βcarotene, and vitamin B12, which play a vital role in inflammatory and immune responses in animals and humans, which promote the macrophages activity and immune cells to increase the production of interferon- γ protein. Therefore, *Amphora* could stimulate the ability of the immune system to fight against pathogens and foreign proteins (Mason, 2001), which were in accordance with (Abdo and Zeinb, 2004), who was indicated that the herbal supplements could improve the immune response since globulin levels were used as an indicator of immune responses and a source of antibody production. Soltan et al. (2008) reported that *Star anise* supplementation in the broiler diet significantly increased lymphocyte counts compared to the control group, possibly be due to an aromatic plant like *Star anise* seeds, which contain many essential B-complex nutritional vitamins such as pyridoxine, niacin, riboflavin, thiamine, and magnesium, copper, potassium, manganese, zinc, and iron. In addition, *Star anise* seeds contained the amounts of antioxidant nutritional vitamins, such as vitamin C and vitamin A (Zhou et al., 2016). Herbal Supplements could

increase the immune response as globulin levels have been used as an indicator of immune responses and antibody sources (Abdo and Zeinb, 2004).

The immunity results were consistent with those of Rahmani and Speer (2005), who found a higher percentage of gamma globulins in broilers given herbal ingredients than the control ones. The present results revealed that there was no significant difference between ALT, AST, Urea, and Creatinine in the treated groups compared to the control group, which indicated that *Amphora* and *Star anise* appeared safe and did not have an adverse effect on physiological and nutritional status. Therefore, the utilization of algae in pharmaceutical applications has attracted world wild attention in recent years (Enwereuzoh and Onyeagoro, 2014). *Star anise* will contribute to the development of more phytotherapeutic products that are cheaper, safer, and affordable, and have a lower risk of resistance than conventional therapeutic drugs (Ritter et al., 2014; Sri et al., 2015).

In the current study, the mRNA expression of GH and IGF-1 was significantly increased in the treated chickens compared to the control chickens ($p < 0.05$). Growth hormones and IGF-1 are required to support normal growth (Scanes, 2009). Furthermore, animal growth is closely related to the mRNA expression levels, as intestinal nutrient transporters are required to circulate digestive products from digestion (McCracken and Edinger, 2013).

The results of the current study are compatible with those of Guobin et al. (2011), who reported that IGFs were important positive modulators of body and muscle growth in mammals and chickens.

In the current study, the splenic mRNA expression of IFN-γ was significantly increased in the treated chickens in comparison with the control chickens and the housekeeping gene. Interferon-γ regulated acquired immunity by stimulating lymphocytes and increasing the expression of class II antigens of Major Histocompatibility (MHC). In addition, IFN-γ is a common marker of cellular immunity, and high levels have been correlated with protective immune responses to parasitic infections (Lee et al., 2008). Interferon-gamma (INF) influences the immune system and inhibits tumor growth, and are involved in various immune interactions as inducers, regulators, and effectors of both innate and acquired immunity during the infections (Priyanka and Muralidharan, 2014).

The molecular results of the present study indicated an increase of INF gene transcription levels in the spleen of the treated chickens compared to the control chickens. Blinkova et al. (2001) reported that algae are important positive stimulators for the production of antibodies, cytokines, and also T and B cell activation. Moreover, the available molecular results from INF agreed with Hirahashi et al. (2002), who reported that algae enhanced Natural killer cell functions by INF- γ production and cytolysis. On the other hand, Mohammed AL (2014) stated a significant increase in the INF-γ concentration in the blood serum of both groups of mice treated with two concentrations of herbal additives (1 and 5 mg/kg BW) compared to the control group. Also, Kim et al. (2010) and Lillehoj et al. (2011) reported that supplementing one-day-old chickens diets with medicinal plants indicated higher rates of interleukin interferon (IFN-γ), encoding gene transcripts in comparison with the chickens given a standard diet.

In the current study, the mRNA expression of the IL-12 levels was significantly increased in the treated chickens compared to the control chickens. These results were in agreement with the results of Philbin et al. (2005), who reported that IL-12 differentiates T cells (Trinchieri, 1994), which is known as a factor that activates T cells, that could promote the T cells growth and function. The activation of T cells enhances IFN-γ development (Lesley et al., 2000). The present finding agreed with Ferdous et al. (2008) and Kirshenbaum et al. (2008), who found that adding the herbal additive to broilers' feed increased the expression of IL–12.

CONCLUSION

The supplementation of *Amphora coffeaeformis* and *Star anise* to the diet of broiler chickens for 35 days was sufficient to improve broiler performance by improving BW, BWG, and FCR and to modulate their immunity through increasing total WBC count, the phagocytic activity percentage, the phagocytosis index in plasma, IgM, and IgG, in serum. In addition,*Amphora* and *Star anise* significantly increased the mRNA expression of the hepatic growth hormone gene, the insulin-like growth factor-1 (IGF-1) genes (IGF1), and the mRNA expression of splenic interferon-gamma (INF-γ), and Interleukin12 (IL-12p35) genes.

DECLARATION

Acknowledgments

We appreciate the Faculty of Veterinary Medicine of the University of Sadat City in Egypt.

Competing interests

The authors declared that they have no conflicts of interest.

Author's contribution

Sherif Mohamed Shawky, Said Ibrahim Fathalla, and Sahar Hassan Orabi have participated in the creation of the conception, design, and writing of the manuscript. Sherif Mohamed Shawky, Said Ibrahim Fathalla, Sahar Hassan Orabi, Huda Hassan El-Mosalhi, and Ibrahim Said Abu-Alya interpreted the data and reviewed the manuscript, while Huda Hassan El-Mosalhi and Ibrahim Said Abu-Alya managed and analyzed the data. Huda Hassan El-Mosalhi, Said Ibrahim Fathalla, and Ibrahim Said Abu-Alya carried out the sampling and management of the samples.

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JWPR
Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 643-648, December 25, 2020

Research Paper, PII: S2322455X2000073-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.73

Seroprevalence of Avian Influenza Virus Subtype H5 among Poultry Workers of Central Traditional Markets in Indonesia

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Received: 04 Nov. 2020
Accepted: 18 Dec. 2020

ABSTRACT

Avian Influenza (AI) has been spread rapidly in almost all the provinces of Indonesia by the end of 2007, and it has become endemic. Avian Influenza viruses can be infecting to human from direct or indirect contact with the infected or dead poultry, and a visit to the wet poultry market in the neighborhood. Seroprevalence studies can be used to identify the clinical key, epidemiological studies, and the spread of AI viruses in humans. The aim of present study was to investigate the seroprevalence of Avian Influenza (AI) virus, subtype H5 among poultry workers at the central traditional market in industrial. To meet the mentioned demand, 26 blood samples were collected from the poultry workers via the median cubital vein. The antibody titer was examined using Hemagglutination Inhibition (HI) assay using H5 antigen from duck licensed under A/Dk/Indonesia/AU-78/12 (H5N1) and three kinds of red blood cells taken from horse, chicken and guinea pig. The serum samples were added with Receptor Destroying Enzyme (RDE) with a ratio of 3:1 (v/v) for an overnight, and pretreated with 10% of red blood cells before the HI assay was conducted. Based on the findings, it can be concluded that the percentage of seroprevalence of Avian Influenza (AI) virus, subtype H5 among poultry workers at central traditional market was 0%. Thirteen samples showed a negative result of the HI test. All of the workers' blood serum obtained less than 2^4 antibody titer from the HI test. As the results showed, the research on the poultry workers in the traditional market was carried out, and it obtained negative results; all the workers were not infected with the Avian Influenza virus. In other words, Avian Influenza is not meaningful in poultry farm workers in Sidoarjo suburb traditional farms.

Key words: Avian Influenza, Poultry workers, Seroprevalence, Traditional market.

INTRODUCTION

Avian influenza (AI), H5N1 is one of the respiratory diseases which commonly affected poultry caused by an influenza virus from the *Orthomyxovirida* family; the virus can also be transmitted to human (Al-Natour and Abo-Shehada, 2005; Wang and Alexander, 2021). The epidemic spread of avian influenza, H5N1 in Indonesia occurred in Java in August 2003 affected birds, which led to the spread of the disease to other areas of south east Asia (Gutiérrez et al., 2009). By the end of 2005, the disease was considered endemic in parts of Java, Sumatra, Kalimantan, Sulawesi, and Bali (Santhia et al., 2009). The first zoonotic transmission was confirmed in western Java in July 2005 (Wiyono et al., 2004; Takano et al., 2009). From then on, a total of 199 human H5N1 cases have been reported, in which 167 were fatal (WHO, 2014). Avian Influenza virus in Indonesia is attributed to H5N1 virus clade 2.1.3 and 2.3.2 (WHO, 2014).

Many researchers have been investigating the spread of AI virus on livestocks, poultry workers, farmers, and their family. Based on the previous study, it was found that influenza A viruse (H5N1) were spread among pigs, and gradually adapted themselves to recognize human-type receptors, affecting farmers, workers, and their families in the farm area to have a great risk of being infected or contaminated with the new viruses (Frederika et al., 2013; Lailirahmawati et al., 2015). The fatality rate of H5N1 was less than the frequent rate reported more than 50%. Although it is impossible to determine H5N1 fatality rate accurately, it could be assumed that 1% to 2% infection rate would translate a large amount of infection in exposed (Wang et al., 2012).

Avian Influenza viruses may be transmitted to human, through direct or indirect contact with the infected or dead poultry, and a visit to wet and non-cleaned poultry markets. The viruses are normally prevented or at least controlled by an immune defense; If the viruses

To cite this paper: Novitasari D and Anwar Ch (2020). Seroprevalence of Avian Influenza Virus Subtype H5 among Poultry Workers of Central Traditional Markets in Indonesia. *J. World Poult. Res.*, 10 (4): 643-648. DOI: https://dx.doi.org/10.36380/jwpr.2020.73

transferred in invading the body and overcoming the immune defenses, they may cause the disease. The viruses will survive and have sufficient time to replicate and transmit the progeny to their host (Xu et al., 2009). Seroprevalence studies have been conducted in Thailand, Cambodia, Vietnam (Dung et al., 2014), and Indonesia (Robert et al., 2010) to evaluate the clinical and epidemiological factors, and other key points related to human influenza A infections (H5N1) in 2011 (Dung et al., 2014).

The researcers were interested to investigate the sero-prevalence of Avian Influenza (AI) virus subtype H5 among poultry workers at a central traditional market in an industrial city in suburb of Sidoarjo. Therefore, the purpose of current study was to investigate the seroprevalence of Avian Influenza (AI) virus subtype H5 whose main habitual activities revolve around poultries in an industrial city's and especially in its central traditional markets.

Ethical approval

The Universitas Airlangga Ethics Committee, Airlangga, approved the employed protocol after the agreement of local health authorities for all participants.

MATERIALS AND METHODS

Collection and the storage procedure of poultry workers' blood serum and red blood cells of horse, guinea pig, and chicken

The blood sample of the workers who worked in the poultry market was taken using an incidental sampling method (Mohsin, 2016).

This research was conducted in a Biosafety Level-2 (BSL-2) laboratory in Avian Influenza Research Center (AIRC), Universitas Airlangga of Indonesia. Implementation of the present research was carried out from February to April 2017. The materials that were used in this research were 26 blood serums from the workers in Larangan Sidoarjo traditional market. The experimental laboratory components were including; duck's AI antigen subtype H5 A/Dk/Indonesia/AU-78/12 (H5N1) from Avian Influenza Research Center (AIRC), 1% and 10% horse Red Blood Cell (RBC), 0.5% and 10% chicken Red Blood Cell (RBC), 0.75% and 10% guinea pig Red Blood Cell (RBC), Phosphate Buffered Saline (PBS) solution, Receptor Destroying Enzyme (RDE) (II) "Seiken" (Denka Seiken Co., Ltd, Tokyo, Japan), physiological saline 0.9%, and alcohol 70%.

Red blood cells used for Hemagglutinin (HA) and Hemagglutinin Inhibition (HI) assay in the current research were taken from horse, chicken, and guinea pig which were collected from cephalic (horse), brachial (chicken), and intracardiac vein (guinea pig) using a syringe, and then were placed into a vacutainer tube with Ethylene Diaminetetra Acetic Acid (EDTA). The preparations of packed RBCs were first started by carefully collecting 3-5 ml blood to be placed into the conical tube by the volume of 15 ml, then filled with cold PBS, and mixed gently by inversion. The mix of RBCs and PBS were centrifuged at 3000 rpm for 5 minutes at 4^{o}C, in which the supernatant was aspirated carefully to not disturb the pellet of RBCs. The conical tube was filled gently with cold PBS again, and the process was repeated carefully for three PBS washes to prevent hemolysis.

On the other hand, Receptor Destroying Enzyme (RDE) treatment was given to remove nonspecific virus inhibitor, which would cause a false positive result in HI assay. First, a vial of RDE (II), Seiken, was reconstituted with 20 ml of 0.9% saline. Three parts of RDE were added to one part of serum (e.g. 20 µl serum + 60 µl RDE), then vortexed for homogenization. The RDE-serum mixtures were incubated at 37^{o}C for 18-20 hours (overnight) in a dry bath, and then heated in a 56^{o}C dry bath for 30 minutes to inactivate the RDE. Following after, the serum was allowed to cool in a room temperature. The 10 ml of RBCs in blood samples of horse, chicken or guinea pig was absorbed (packed RBCs) according to the procedure to remove the nonspecific agglutinin (WHO, 2013). One part of RBCs 10% was combined with one part of treated serum (e.g. 20 µl serum + 60 µl RDE + 80 µl RBCs 10%). It was mixed thoroughly and incubated at room temperature for 30 minutes, then inverted gently to be mixed every 10 minutes. The treated serums were centrifuged at 2000 rpm for 10 minutes at 4^{o}C to pellet the erythrocytes. The serum was decanted and placed in another Eppendorf to be tested in HI assay, then the erythrocytes pellet was discarded (WHO, 2013; Born et al., 2019).

Hemagglutinin assay and hemagglutinin inhibition assay with red blood cells of the horse, chicken, and guinea pig

The blood samples were taken from 24 male animals contained 4 horses, 12 chickens, and 8 guinea pigs and Hemagglutinin (HA) assay was done. The determination of HA titers of AI antigen subtype H5 (separated from animals' blood) was carried (IDVet Kit, ID Screen® Influenza H9 Elisa Antibody kit, France). The concentrate

of red blood cells was 1%, and it was put on "V-bottom" microplate (Wang et al., 2014). First, 50 µl of PBS were added to 12 wells in rows A and B (control RBC). Then, 50 µl of the antigen added to well A1. Serial of two-fold dilutions were made by transferring 50 µl from well A1 sequentially through well A12, then 50 µl were discarded from well A12. Fifty µl of 1% suspension of each kind of RBC was added to all wells in rows A and B. The plate was tapped gently to be mixed and covered with plastic wrap, then incubated at room temperature for 60 minutes. After that, the haemagglutination assay (HA) titer was read by tilting the plate at 45^o to 60^o angle. The settled RBCs in row B (control RBC) would start running, and formed a teardrop-shape due to the gravity, and the result was positive if the erythrocytes formed a diffuse film. Antigen titer was the highest dilution of virus that still caused complete hemagglutination (Born et al., 2019).

The standard working dilution of virus must have an HA titer of eight hemagglutination units (HAU) per 50 µl (as same as four HAU per 25 µl). If the working antigen did not have an HA titer of eight HAU per 50 µl, it must be adjusted accordingly to the titer of antigen by diluting the virus with PBS to decrease the number of HAU. For instance, prepared three ml of eight HAU per 50 µl from 2^4 HA titer was done by adding 1.5 ml antigen with 1.5 ml PBS. Therefore, the diluted viruses that contained eight HAU per 50 µl (or four HAU per 25 µl) must be verified by performing a second HA test/retitration (WHO, 2013). The retritration or back titration was a procedure to verify the correct units of hemagglutinin. The retitration process was carried out for each kind of red blood cells.

Besides, HI assay was also investigated for each kind of RBCs from horse, chicken, and guinea pig. Hemagglutinin assay in this research was used RBCs 1% and "V-bottom" microplate for each type of RBCs source was applied respectively. First, 25 µl of PBS were added to the well number 1 to 12. Then, 25 µl of treated serum was added to the well number 1, and serial of two-fold dilutions were made by transferring 25 µl from the first well to the well number 10. The final 25 µl were discarded. After that, 25 µl of standardized antigens containing four HAU were added to all wells containing the serum (except well number 11 and 12), and 25 µl of PBS was added to all wells in column number 11 to be used as RBC controls and all wells in column number 12 for serum control. The plate was tapped gently to be mixed and covered with plastic wrap, then incubated at room temperature for 30 minutes.

After that, 50 µl of 1% horse RBC suspension was added to each well. The plate was tapped gently to be mixed and covered with plastic wrap, then incubated at room temperature for 60 minutes. The HI titers of the serums were recorded after the 60 minutes of incubation by tilting the plate at a 45^o to 60^o angle. The settled RBCs in column number 11 should start pulling or running, and they formed a teardrop-shape due to the gravity. Antibody titer is the reciprocal of the antiserum's highest dilution that produces complete hemagglutination inhibition. Positive antibody titer is a sample that has higher or equal titer with 2^4 (15,18). The data from HI assay was presented descriptively by calculating the percentage of the antibody of AI virus subtype H5 among the workers in the poultry market.

RESULTS

Collection and storage procedure of the workers' blood serum, red blood cells of horse, guinea pig, and chicken

Based on the result of present study, 13 samples have been collected from blood serums of the workers at the Larangan traditional market in Sidoarjo, Indonesia. Red blood cells that were used for HA and HI assay in this research were from the horse, chicken and guinea pig. They were collected from the cephalic (horse), brachial (chicken), and intracardiac (guinea pig) veins. Present study succeeded in taking the samples according to the criteria of the existing procedures (WHO, 2013). All samples used in the current study were feasible and appropriate for the HA and HI test. All samples of red blood cells were collected; HA and HI assays were performed, and the data was analyzed and presented descriptively.

Hemagglutinin assay and hemagglutinin inhibition assay with the red blood cells of horse, chicken, and guinea pig

Based on the result of this study, the researchers used three different kinds of RBCs in HI test, which were from horse, guinea pig, and chicken to be compared and given a more sensitive result to detect human AI, and AI subtype H5 antigen from duck A/Dk/Indonesia/AU-78/12 (H5N1). From 13 serum samples, any evidence of positive antibodies titer was found against AI subtype H5 among the workers in the central traditional market in the industrial city of Sidoarjo, Indonesia, therefore the seroprevalence was 0% (Table 1).

Table 1. The results of hemagglutination inhibition test for the workers on avian influenza subtype H5 using RBCs of horse, guinea pig, and chicken

No.	Serum code	RBCs			Statement
		Horse	Guinea pig	Chicken	
		HI test result (antibody titer)			
1	LSR 1	$< 2^4$	$< 2^4$	$< 2^4$	Negative
2	LSR 2	$< 2^4$	$< 2^4$	$< 2^4$	Negative
3	LSR 3	$< 2^4$	$< 2^4$	$< 2^4$	Negative
4	LSR 4	$< 2^4$	$< 2^4$	$< 2^4$	Negative
5	LSR 5	$< 2^4$	$< 2^4$	$< 2^4$	Negative
6	LSR 6	$< 2^4$	$< 2^4$	$< 2^4$	Negative
7	LSR 7	$< 2^4$	$< 2^4$	$< 2^4$	Negative
8	LSR 8	$< 2^4$	$< 2^4$	$< 2^4$	Negative
9	LSR 9	$< 2^4$	$< 2^4$	$< 2^4$	Negative
10	LSR 10	$< 2^4$	$< 2^4$	$< 2^4$	Negative
11	LSR 11	$< 2^4$	$< 2^4$	$< 2^4$	Negative
12	LSR 12	$< 2^4$	$< 2^4$	$< 2^4$	Negative
13	LSR 13	$< 2^4$	$< 2^4$	$< 2^4$	Negative

Antibody titers might be regarded as positive if there is inhibition at a serum dilution of 1/16 or $\geq 2^4$ (OIE, 2014). LSR is a code for coding samples.

DISCUSSION

The purpose of the current study was to investigate the seroprevalence of Avian Influenza (AI) virus, subtype H5 among the workers in the central traditional poultry market of Sidoarjo, Indonesia. According to this research, none of the sample had a positive result (0%), nor indicated the existence of AI virus even though previous investigation which revealed that the wild birds around Larangan traditional market in Sidoarjo were infected with AI virus H5N1 (Poetranto et al., 2011). Other previous research also reported that there was a report of AI virus subtype H5 in Larangan traditional market of Sidoarjo (Frederika et al., 2013; Lailirahmawati et al., 2015). Therefore, the researchers assumed that the zero seroprevalence might be due to no avian-to-human transmission yet in the central traditional market of Larangan, Sidoarjo, Indonesia.

Avian-to-human transmission is limited and rare because the species barrier is quite strong to accommodate the transmission of H5N1 virus. Through the use of lectins Maackia amurensis agglutinin (MAA) for *SAα2,3Gal* receptors and Sambucus nigra agglutinin (SNA) for SAα2,6Gal receptors, it was discovered that avian and human influenza viruses typically have a different SA-binding preference. Therefore, host range distribution is strongly restricted by the receptor specificity due to the surface antigen of hemagglutinin (HA) protein. Human influenza viruses bind preferentially to *SAα2,6Gal* receptors which is dominantly located on epithelial cells in the upper respiratory tract of human (i.e. H1N1 and H3N2 viruses), but H5N1 viruses bind preferentially to SAα2,3Gal receptors, whereas it is predominantly located in the low respiratory tract of humans such as type II pneumocytes, alveolar macrophage, and non-ciliated cuboidal epithelial cells in terminal bronchioles. The result of this condition was the no replication of the virus due to the failure of the virus to recognize and attach to the receptors. Hence, this different distribution of the receptors might limit the H5N1 virus to infect human easily, moreover through human-to-human transmission. Zoonotic transmission of H5N1 might only occur when the virus mutated and acquired the ability to recognized SAα2,6Gal receptors besides SAα2,3Gal receptors (Shinya et al., 2006; De Graaf and Fouchier, 2014).

The negative result might also be the cause of the small number of exposures or contact with the virus. Even though poultry workers often make a contact with the dead or infected chicken or more intensive poultry exposure, and are expected to have a higher risk of infection due to the lack of preventive measures and healthy environment, it does not mean that the poultry workers must have positive antibody against Avian Influenza subtype H5 (Indriani et al., 2010; Huo et al.,

2012). besides poultry workers that are prone to AI infection, others are people who visit the wet market. However, the people do not have constant exposure or direct contact with the infected poultry. Despite of that, a lot of AI-infected cases of people who visit the wet market were acute and fatal (To et al., 2012). This might happen when the people were exposed to a high amount of virus, but did not have a good body condition, which led to a bad immune response. Avian influenza A (H5N1) in humans differs in multiple ways from the influenza as a human virus, including the routes of transmission, clinical severity, pathogenesis, and response to treatment (Kumar et al., 2018).

The result of negative inhibition test occurred is the HI reference reagent as antigen was not antigenetically related to the serum (Kumar et al., 2018). Avian Influenza virus is an RNA virus which can easily mutate. Therefore, there was a possibility where the virus was mutating into a new form and structure. The serums which the researcher used were also mostly from the poultry workers at Larangan traditional market in which the majority of the tenants sell chicken, while the antigen for this research's HI assay was using antigen originated from the duck. Furthermore, the clade of the Avian Influenza subtype H5 antigen used was clade 2.3.2, while the highest cumulative number of avian-to-human transmission for H5NI cases and death in Indonesia was caused by Avian Influenza A subtype H5 clade 2.1.3 (Yupiana et al., 2010). These differences between species and the HA phylogeny also might be contributed to the negative result. Another reason that might also affect the results was that the antigen was taken from avian influenza outbreak in 2012. Therefore, there was a possibility that the virus circulating at Larangan traditional market in Sidoarjo was not the same as the one in the outbreak in 2012. Giving interventions directly in poultry sector was the most effective way to prevent human HPAI (Yupiana et al., 2010).

This study still had some limitations such as the lack of observations that can complement the results of research on the biological characteristics of the condition of poultry workers who contracted the AI virus, no microscopic observations of blood cells infected with the AI virus, and comparison of the seropositive clade type was not done. However, the results of the current study have provided additional information that poultry workers in the central traditional market of Sidoarjo were not infected with the Avian Influenza virus. Poultry workers in the market need to be given further precautions and safeguards against AI viruses. This research can be useful for veterinarians, practitioners, breeders, poultry workers, scientists, and livestock entrepreneurs as a prevention towards the poultries from spreading the AI virus.

CONCLUSION

Based on results of the research, it can be concluded that the percentage of seroprevalence of Avian Influenza (AI) virus subtype H5 among poultry workers at the central traditional market in Sidoarjo was 0%, which means that none of the workers tested were contaminated with AI virus subtype H5.

DECLARATION

Competing interests

All authors have no conflict of interest to declares

Author`s contribution

Dina Novitasari and Chairul Anwar had similar roles in conduction and collection of samples and data, as well as analysis of data. Both authors checked and approved the final version of the manuscript.

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Journal of World's Poultry Research

2020, Scienceline Publication

J. World Poult. Res. 10(4): 649-661, December 25, 2020

Research Paper, PII: S2322455X2000074-10
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DOI: https://dx.doi.org/10.36380/jwpr.2020.74

Characterization and Analysis of the Major Structural Protein Genes of the Recently Isolated Avian Infectious Bronchitis Virus in Egypt

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Received: 09 Nov. 2020
Accepted: 21 Dec. 2020

ABSTRACT

Infectious Bronchitis Virus (IBV) is a severe infectious disease affecting chickens and causing serious economic loss. Although several studies have been conducted to characterize HVRs-S1 (Hyper-Variable Regions of Spike 1 gene) in Egypt, few of which aimed to characterize the major structural protein genes. In the present study, the genetic characterization of the major structural protein genes was carried out in 10 isolates selected from six governorates in 2019. Phylogenetically, the S1 gene was clustered into genotype GI-23 (variant II), with seven viruses that were clustered into Egy/Var II occurring in two subgroups (I, II) when aligned with previously isolated Egyptian strains. It had a specific character of 40 Amino Acids (AA) mutations except for IBV/EG/CV32/2019, which had 50 AA mutations, specifically in HVRs regions (HVRI, II, and III). The other three strains were clustered into Egy Var I with 17 AA mutations except IBV/EG/F859/ 2019, which had 15 AA mutations, compared to IBV/CU/4/2014 reference strain. The examined isolates had an additional glycosylation site at position 280 and one was missing at position 139 with the exception of two strains that only had an additional one, compared to IBV/CU/4/2014. The viruses in this study differed genetically from various vaccine seeds in the range of 69-83%. The Nucleocapsid, genetically characterized in the group of variant II (Egy/Var II) and the glycoprotein membrane genes genetically characterized in the variant group in a new sub-group with 11 and 9 AA mutations, respectively. The recombination event was only detected in the S1 gene in two isolates of IBV/EG/CV32/2019 and IBV/EG/F859/2019 from D274 and QX, respectively. In this regard, it is important to conduct continuous surveillance, pathogenicity study, and vaccine efficacy evaluation.

Keywords: Characterization, Infectious bronchitis virus, Major structure protein, Matrix, Nucleoprotein, Spike

INTRODUCTION

Infectious bronchitis virus (IBV) is a serious viral disease affecting poultry and causing high economic loss worldwide (Cavanagh et al., 2007; Milek et al.,2018). It is caused by avian IBV, a member of the *Coronaviridae* family, the 99+*Coronavirinae* subfamily and genus *Gammacoronavirus* (Carstens, 2009). It affects the respiratory, reproductive, and renal systems of all ages in different ways and increases the exposure to other pathogen infections (Cavanagh et al., 2007; Jackwood, 2012).

The IBV genome is a single-stranded and positive-sense (Masters and Perlman, 2013). The genome consists of 5 ′-UTR-1a-1b-S-3a-3b-E-M-4b-4c-5a-5b-N-6b-UTR-poly (A) tail-3′ (Brierley et al., 1989) encodes major structural proteins and non-structural protein. The major structural protein is composed of glycoprotein Spike (S), Nucleocapsid (N) protein, glycoprotein Membrane (M), and protein Envelope (E) (Thor et al., 2011; Wang et al., 2017)

The S glycoprotein is a surface protein cleaved into two subunits of S1 and S2. The S1 subunit constitutes the highly variable globular head, which was responsible for the serotype and virus neutralization (Cavanagh et al., 1992). In addition, it contains a receptor binding site that is important for tissue tropism (Ammayappan et al., 2009). The N protein plays a significant role in the replication and assembly of the virus (Lai and Holmes, 2001). The S1 and N are the key genes for determining pathogenicity, evolution, and diversity of IBV (Lee et al., 2003; Ammayappan et al., 2009). The M protein is mainly responsible for the viral assembly process (Corse and Machamer, 2003). Several IBV serotypes and genotypes

with minimal cross-protection were found around the world. The IBV evolves rapidly in nature through the substitution, insertion, deletion and/or recombination of different genes (Jackwood, 2012; Hewson et al., 2014; Hassan et al., 2019). Thus, the new highly virulent viruses emerge with minimal cross-protection leading to vaccination failure (Cavanagh et al., 2007; Jackwood, 2012). Multiple serotypes and genotypes of IBV were found in Egypt and co-circulated in the field (Abdel-Moneim et al., 2002; Abdel-Moneim et al., 2012). Depending on the complete S1 sequence, Valastro et al (2016) grouped the Egyptian variant strains into the GI-23 lineage. An Egyptian variant I strain was identified in various poultry farms in 2001 (Abdel-Moneim et al., 2002). In 2011, the new variant (Egyptian variant II) was detected in both vaccinated and non-vaccinated flocks causing severe outbreaks (Abdel-Moneim et al., 2012). The Egyptian variant II differed from the classical vaccine H120 and Ma5 used in Egypt (Abd El Rahman et al., 2015). In 2012, an upgrade of the vaccines was introduced to control the outbreak in Egypt using "variant" vaccine strains 1/96, 4/91, CR88, and D274 (Abozeid et al., 2017). With this background in mind, the present study aimed to investigate the variability of major IBV structural protein genes in Egypt (S1, N, and M) during 2019 using 10 isolates from different governorates and evaluate current control measures in the field.

MATERIALS AND METHODS

Ethical approval

The present study did not work on animals or human participants directly.

Isolation information

In the present study, ten IBV isolates from ten infected chicken farms from six different governorates were isolated in 2019 in nine to 11-days-old Specific Pathogenic Free Embryonated Chicken Egg (SPF-ECE) in the allantoic fluids and then the allantoic fluid was collected after 48 hours post-inoculation and stored at -80 °C (Li et al., 2012). The S1, N, and M genes were sequenced and published by the National Center for Biotechnology Information (NCBI) with the accession number provided in Table1.

Polymerase chain reaction and sequencing of S1, N, and M genes from IBV isolates

Viral RNA was extracted from the infected allantoic fluid of Specific Pathogen Free (SPF) eggs using a mini kit of QIAmp viral RNA (Qiagen, Hilden, Germany), as instructed by the manufacturers. The cDNA synthesis was performed using a First-Strand Synthesis System SuperScriptTM III (Thermo Fisher Scientific, MA, USA) according to the manufacturer's instructions. The S1, N, and M genes were amplified using specific primers (Table 2) and high fidelity Phusion® DNA polymerase (Thermo Fisher Scientific, MA, USA) according to the manufacturer protocol. The amplification of the reverse transcription-Polymerase Chain Reaction (PCR) were detected by agarose gel electrophoresis. The purification was carried out using the QIAquick Gel Extraction Kit (Qiagen, Hilden, Germany). Full-length sequencing was performed with gene-specific primers using a BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, California, USA) and the nucleotide sequence was obtained from an ABI 3500 Genetic Analyzer (Life Technologies, California, USA).

Table 1. Epidemiological data and accession number of major structural protein genes (S1, N, and M) of IBV isolates by the National Center for Biotechnology Information

	Code	collection Date	Governorate	GenBank Accession number		
				S1	N	M
1	IBV/EGY/CH/CV48/2019	2/2019	Giza	MN651560	MT085346	MT085356
2	IBV/EGY/CH/CV10/2019	1/2019	Sharqia	MN651561	MT085342	MT085359
3	IBV/EGY/CH/CV17/2019	5/2019	Behera	MN651562	MT085343	MT085358
4	IBV/EGY/CH/CV31/2019	5/2019	Sharqia	MN651563	MT085344	MT085353
5	IBV/EGY/CH/CV32/2019	3/2019	Behra	MN651564	MT085349	MT085352
6	IBV/EGY/CH/CV125/2019	1/2019	Giza	MN651565	MT085347	MT085354
7	IBV/EGY/CH/F580/2019	7/2019	Dakhlia	MN651566	MT085345	MT085361
8	IBV/EGY/CH/F564/2019	6/2019	Qaliobia	MN651567	MT085348	MT085360
9	IBV/EGY/CH/F742/2019	4/2019	Gharbia	MN651568	MT085350	MT085357
10	IBV/EGY/CH/F859/2019	8/2019	Sharqia	MN651569	MT085351	MT085355

Table 2. Primers sequences of S, N, and M genes of IBV

Gene	Primer sequence		Amplicon size	Reference
NP	3' NP-F 3'NP-IR	ATTCCAAGGGAAAACTTGTG TCCTCATTCATCTTGTCATCACC	832	The present study
	NP-IF NP-R	GGTATAGTGTGGGTTGCTG AGCTGTGCATTGTTCCTCTC	832	The present study
M	3'M-F 3'M-R	TTTTGGTATACATGGGTAG TACTCTCTACACACACACAT	880	The present study
S1	IBV-S1- F2 IBV- HVR3- Reverse	GATTGTGCATGGTGGACAATG CAGAYTGCTTRCAACCACC	1100	Abdel-moneim et al. (2002); Naguib et al. (2017)
	IBV-HVR3- Forward IBV-Oligo -3-Reverse	TACTGGTAATTTTTCAGATGG CATAACTAACATAAGGGCAA	900	Adzhar et al. (1997); Gelb et al. (2005)

Genetic and phylogenetic analysis

Nucleotide and amino acid sequences of ten isolates were alignments with other IBV strains representing different groups (classical, variant I, variant II) and vaccine seeds (H120, M41, Ma5, 4/91, CR88121, and D274) that were used in Egypt were obtained from the National Center for Biotechnology Information. The alignment was carried out with the CLUSTAL-W program and the MegAlign module of DNASTAR software (Lasergene version 7.2; DNASTAR, Madison, WI, USA). The phylogenetic tree was constructed using MEGA version 6 (Tamura et al., 2013) according to the maximum likelihood tree method with moderate strength and 1000 bootstrap replicates (Kumar et al., 2016). The pairwise nucleotide percent identity was calculated using DNA star software (DNAStar, Madison, WI). The glycosylation sites were detected using NetN-Glyc 1.0 Server (Gupta et al., 2004).

Estimation of selection pressure

The sequence of S gene from the ten isolated IBV was analyzed to determine the selection pressure for each gene segment by estimating the ratio of non-synonymous (dN) to synonymous (dS) substitutions ($\omega = dN/dS$) across the lineages towards a codon-by-codon basis. The selective pressure was defined as $\omega = 1$ indicates a neutral evolution, $\omega < 1$ denotes a negative or purifying selective pressure, and $\omega > 1$ refers to a positive selective pressure. The mean values of ω were calculated using the SLAC and FEL methods on the Datamonkey website (Delport et al., 2010).

The Recombination Detection Program (RDP 4, Version 4.95) was used to identify possible recombination events of S1, M, and N genes (Mo et al., 2013), including the algorithms RDP, Bootscan, Geneconv, MaxChi, Chimaera, SiScan, and 3Seq (Martin et al., 2015).

RESULTS

Genetic characterization of the spike gene

Phylogenetic analysis of the spike gene revealed that the ten Egyptian strains were clustered in GI 23 (variant II). The findings indicated that seven out of ten strains were clustered into Egy Var II, divided into two sub-groups (I, II) as shown in Figure 1. The spike gene had specific features, compared to the reference strain IBV/CU/4/2014 isolated from Egypt in 2014. It had 40 Amino Acid (AA) mutations with the exception of IBV/EG/CV32/ 2019 that had a specific character with 50 AA mutations in different sites. The other three strains were clustered to Egy Var I with specific features. The three strains had 17 AA mutations with the exception of IBV/EG/F859/ 2019 that had 15 AA in comparison with the reference strain IBV/CU/4/2014 isolated from Egypt in 2014.

Hypervariable Regions (HVRs) in the S1 gene demonstrated different patterns among different viruses, compared to the IBV/CU/4/2014 strains. All of the Egy Var II related strains in the new cluster had two, four, and eight AA mutations with the exception of IBV/EG/cv32/ 2019 with 6, 7, 8 AA mutations in the HVRI, II, III, respectively (Figure 2).

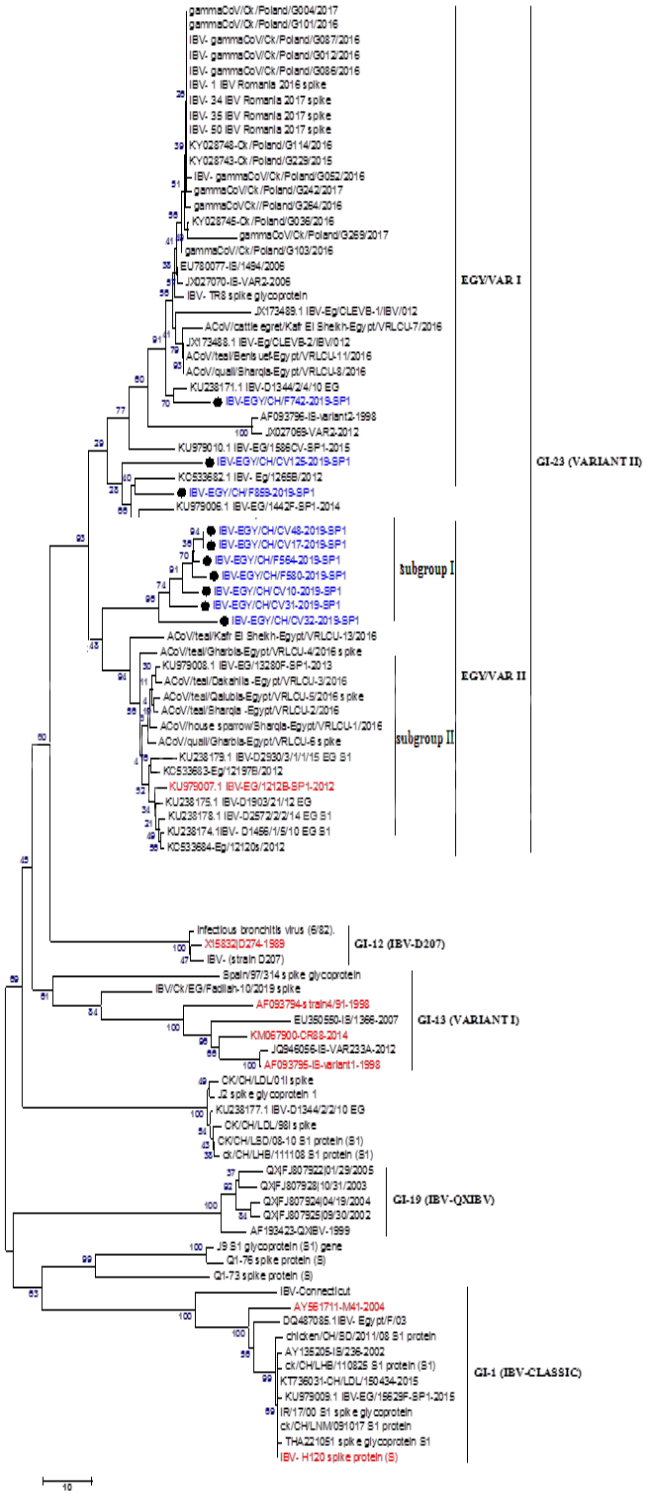

Figure 1. Phylogenetic tree of the S1 gene. Figure shows the phylogenetic analysis of the S1 gene indicating all Egyptian strain clusters into genotype GI-23 (variant II) with three strains were sub-clustered into Egy VAR I and the other seven isolates sub-clusters into Egy VAR II, dividing it into two subgroups (I, II). Black dots indicate viruses sequenced in the current study.

The other three strains related to Egy Var I had two AA mutations in the HVRI with the exception of IBV/EG/F859/ 2019 which had one AA mutation. The four AA mutations were detected in the HVRII, except that IBV/EG/F742/ 2019 with three AA mutations. Finally, HVRIII of IBV/EG/CV125/ 2019, IBV/EG/F859/ 2019, IBV/EG/F742/ 2019 had five, seven, and one AA mutations, respectively (Figure 2).

All of the IBV strains in the present study had 17 N-linked glycosylation sites. However, the isolated strains lacked the glycosylation site at position 139 and had an additional glycosylation site at AA 280, compared to IBV/CU/4/2014 reference strain with the exception of IBV/EG/F742/2019 and IBV/EG/CV32/2019, which had an additional one at only 280. Selection pressure analysis demonstrated five positive selections at position 53, 69,128, 232, and 262 in all strains of the S1 gene.

Phylogenetic analysis and amino acids identity of the S1 gene revealed that the variant IBV isolates (Egy/Var I and Egy/Var II) had a significant relationship with vaccine seeds commonly used in Egypt, including H120, M41, 4/91, CR88, D274, Var I 1/96, in the range of 69% to 83% (Table 3).

Genetic characterization of N gene

Phylogenetic analysis of the N gene classified IBV strains into classical and variant groups. The variant group was classified into variant I and variant II. The Egyptian strains in the present study were clustered in GI 23 variant II and divided into two sub-groups (I, II; Figure 3). All strains had specific features (16 AA mutations), compared to the reference strain IBV/CU/4/2014 isolated from Egypt in 2014. However, the IBV/EG/CV32/ 2019 had a specific character with 11 AA mutations at different sites with no selection pressure. The amino acid identity of the N gene of the 10 strains, compared to IBV vaccine seeds Egypt, including Ma5, H120, 4/91, CR88, ranged 91-95% (Supplementry Table 1). All strains presented one N-glycosylation site at N protein residue 32 (Site of glycosylation: NASW).

Genetic characterization of M gene

The phylogenetic analysis of the M gene revealed no differentiation between variant I and II. All isolated strains in the present study were clustered in the variant group and appeared in a new sub-group (Figure 4). All of the strains had nine AA mutations, compared to the reference strain IBV/CU/4/2014 isolated from Egypt in 2014 without any selection pressure. The nucleotide identity of the M gene of the ten strains, compared to IBV vaccine seeds IBV/H120, Ma41, 4/91, was within the range of 94-96% (Supplemntry Table 2). All strains showed only one N-glycosylation site at residue 3/4/6 (Site of glycosylation: NCTL).

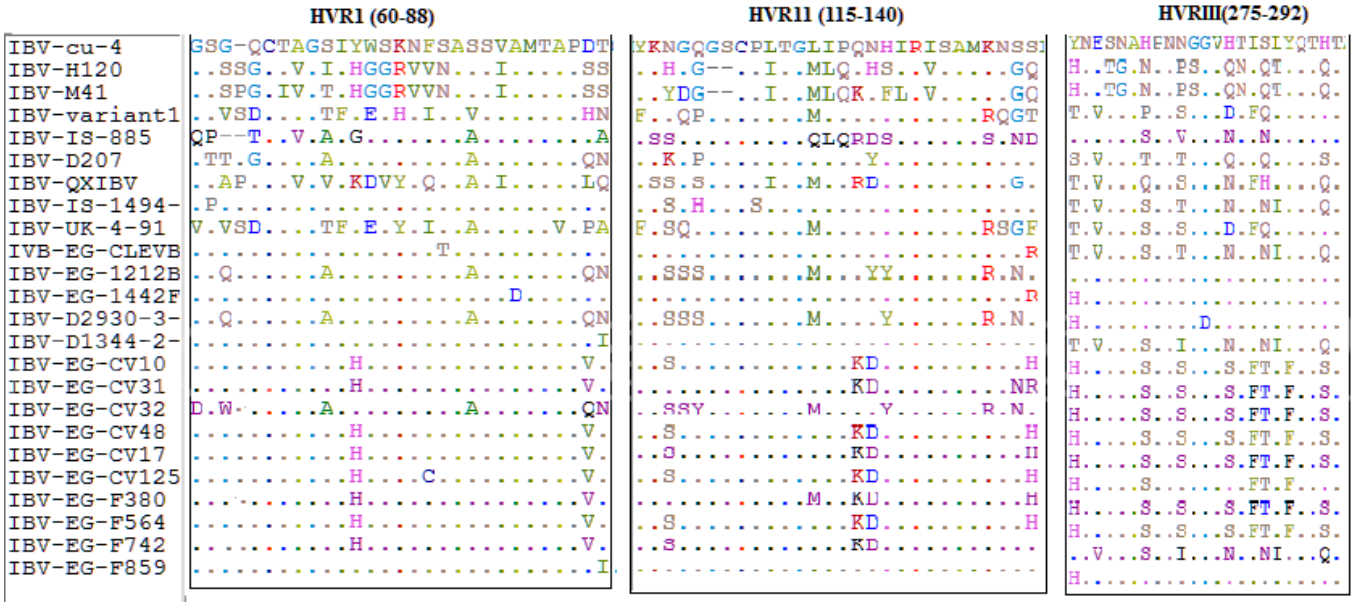

Figure 2. Hyper-variable regions of the S1 gene of IBV. The amino acid alignment and mutation of hyper-variable regions of tested isolates, compared to IBV/CU/4/2014.

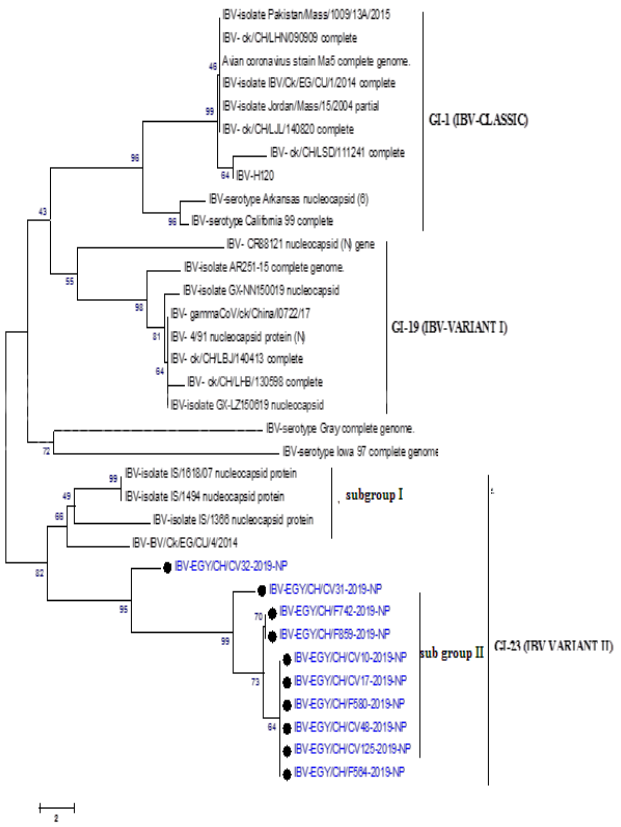

Figure 3. Phylogenetic tree of the N gene. The phylogenetic analysis of the N gene revealed that all Egyptian strain clusters into genotype GI-23 (variant II) divided it into two subgroups (I, II). Black dots indicate viruses that were sequenced in the current study.

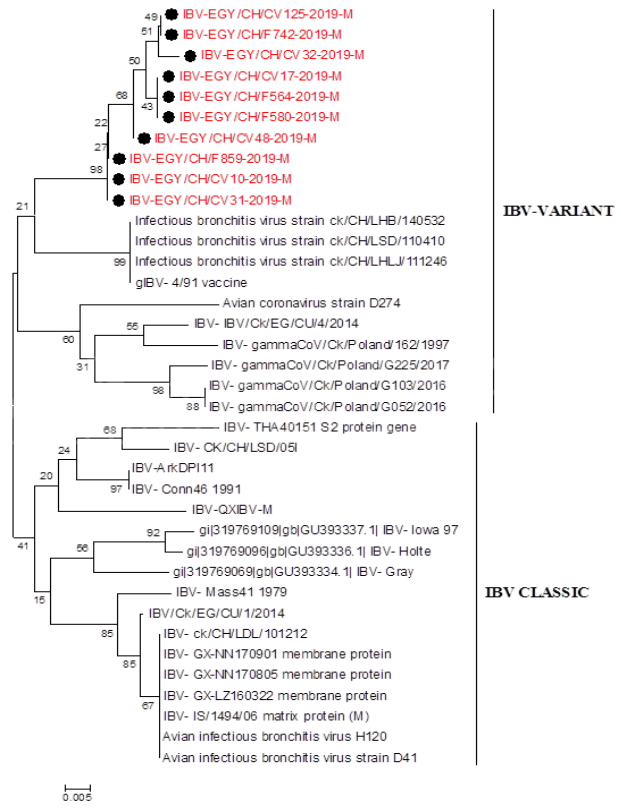

Figure 4. Phylogenetic tree of M gene. The phylogenetic analysis of the M gene revealed that all Egyptian strain clusters into the variant group in a new subgroup. Black dots indicate viruses that were sequenced in the current study.

Table 3. Nucleotide and Amino acid identities and divergence of S1 gene sequenced viruses compared to other selected strains and vaccine strains. Comparative alignment of the S1 gene showed that S1 A.A identity percent of tested strain ranged 69% to 83% with different vaccine seeds used in Egypt.

Sequence name	Ck/EG/CU/4/2014	EU780077-IS/1494/2006	IS/885-2003	D274-1989	AY561711-M41-2004	IBV-EG/1212B-SP1-2012	IBV-Eg/CLEVB-2/IBV/012	IS-variant1-1/96	IS-VAR2-2006	QXIBV-1999	IBV-Connecticut	IBV- (strain D207)	IBV- H120	CR88121-2014	AF093794-strain4/91-1998	IBV-EGY/CH/CV10-2019-SP1	IBV-EGY/CH/CV31-2019-SP1	IBV-EGY/CH/CV32-2019-SP1	IBV-EGY/CH/CV48-2019-SP1	IBV-EGY/CH/CV17-2019-SP1	IBV-EGY/CH/CV125-2019-SP1	IBV-EGY/CH/F580-2019-SP1	IBV-EGY/CH/F564-2019-SP1	IBV-EGY/CH/F742-2019-SP1	IBV-EGY/CH/F859-2019-SP1
	NUCLEOTIDE IDENTITY %																								
1. Ck/EG/CU/4/2014		95%	88%	83%	80%	95%	95%	79%	95%	78%	79%	83%	80%	79%	79%	93%	90%	84%	93%	93%	93%	93%	90%	94%	97%
2. IS/1494/2006	94%		88%	83%	80%	91%	99%	79%	100%	78%	79%	83%	80%	79%	80%	93%	88%	84%	93%	93%	91%	92%	90%	98%	94%
3. IS/885-2003	88%	88%		80%	79%	88%	88%	78%	88%	78%	78%	80%	79%	78%	79%	87%	83%	80%	87%	87%	85%	87%	84%	88%	88%
4. D274-1989	83%	84%	80%		80%	84%	83%	79%	83%	78%	79%	98%	80%	79%	79%	82%	79%	78%	82%	82%	79%	82%	79%	82%	82%
5. M41-2004	76%	75%	74%	77%		79%	80%	78%	80%	78%	95%	80%	97%	78%	78%	79%	76%	73%	79%	79%	76%	79%	76%	79%	79%
6. IBV-EG/1212B-SP1-2012	94%	90%	87%	84%	75%		91%	79%	91%	78%	78%	84%	79%	78%	78%	90%	88%	87%	89%	89%	89%	90%	86%	91%	95%
7. IBV-Eg/CLEVB-2/IBV/012	94%	99%	87%	83%	75%	90%		80%	99%	78%	79%	83%	80%	79%	80%	93%	88%	84%	93%	93%	91%	92%	90%	98%	94%
8. IS-variant1-1/96	79%	79%	77%	78%	74%	78%	79%		79%	78%	77%	79%	77%	97%	96%	78%	75%	73%	78%	78%	76%	79%	76%	78%	78%
9. IS-VAR2-2006	94%	100%	87%	83%	74%	90%	98%	79%		78%	79%	83%	80%	79%	79%	93%	88%	84%	93%	93%	91%	92%	90%	98%	94%
10. QXIBV-1999	78%	79%	79%	78%	77%	78%	79%	78%	78%		78%	78%	79%	79%	80%	78%	75%	73%	77%	78%	75%	77%	75%	78%	77%
11. IBV-Connecticut	76%	75%	75%	78%	91%	75%	75%	74%	75%	76%		79%	94%	77%	78%	78%	75%	73%	78%	78%	75%	78%	75%	78%	78%
12. IBV- (strain D207)	83%	83%	79%	98%	76%	84%	83%	78%	83%	78%	77%		80%	79%	79%	82%	79%	78%	82%	82%	79%	82%	79%	82%	82%
13. IBV- H120	77%	75%	76%	77%	96%	76%	76%	74%	75%	78%	91%	78%		77%	78%	79%	76%	73%	79%	79%	76%	79%	76%	79%	79%
14. CR88121-2014	79%	80%	76%	79%	74%	77%	80%	96%	79%	79%	74%	79%	74%		97%	78%	75%	73%	78%	78%	76%	79%	76%	78%	78%
15. AF093794-strain4/91-1998	78%	79%	78%	79%	74%	77%	79%	93%	79%	80%	74%	78%	75%	94%		78%	76%	73%	79%	79%	76%	79%	76%	79%	78%
16. IBV-EGY/CH/CV10-2019-SP1	92%	91%	86%	82%	74%	89%	91%	78%	91%	78%	74%	82%	74%	78%	78%		95%	89%	99%	99%	92%	99%	96%	94%	93%
17. IBV-EGY/CH/CV31-2019-SP1	88%	87%	83%	79%	72%	87%	87%	75%	86%	76%	72%	79%	73%	76%	76%	94%		93%	94%	94%	94%	94%	98%	90%	91%
18. IBV-EGY/CH/CV32-2019-SP1	84%	82%	80%	77%	69%	86%	82%	72%	82%	73%	70%	76%	69%	73%	73%	89%	92%		88%	89%	87%	89%	92%	84%	85%
19. IBV-EGY/CH/CV48-2019-SP1	91%	91%	86%	81%	74%	89%	91%	78%	91%	78%	74%	81%	74%	79%	78%	99%	94%	88%		100%	92%	99%	96%	94%	92%
20. IBV-EGY/CH/CV17-2019-SP1	91%	91%	86%	81%	74%	89%	91%	78%	91%	78%	74%	81%	74%	79%	78%	99%	94%	88%	100%		92%	99%	96%	94%	92%
21. IBV-EGY/CH/CV125-2019-SP1	91%	89%	84%	79%	72%	88%	89%	75%	89%	76%	72%	79%	73%	75%	75%	91%	93%	86%	92%	92%		91%	94%	92%	93%
22. IBV-EGY/CH/F580-2019-SP1	91%	90%	86%	81%	74%	89%	91%	79%	90%	78%	74%	81%	75%	79%	79%	98%	94%	88%	99%	99%	91%		96%	93%	92%
23. IBV-EGY/CH/F564-2019-SP1	88%	88%	82%	78%	71%	85%	87%	75%	87%	76%	72%	78%	72%	76%	76%	95%	97%	91%	96%	96%	94%	96%		91%	89%
24. IBV-EGY/CH/F742-2019-SP1	92%	96%	87%	82%	74%	89%	96%	78%	96%	78%	74%	82%	75%	79%	78%	92%	88%	82%	93%	93%	91%	92%	89%		94%
25. IBV-EGY/CH/F859-2019-SP1	97%	94%	87%	83%	75%	94%	94%	78%	93%	78%	75%	83%	76%	78%	78%	92%	90%	84%	91%	91%	92%	91%	88%	93%	
	AMINO ACIDS IDENTITY %																								

To cite this paper: Yehia N, Said D and Zanaty AM (2020). Characterization and Analysis of the Major Structural Protein Genes of the Recently Isolated Avian Infectious Bronchitis Virus in Egypt. *J. World Poult. Res.*, 10 (4): 649-661. DOI: https://dx.doi.org/10.36380/jwpr.2020.74

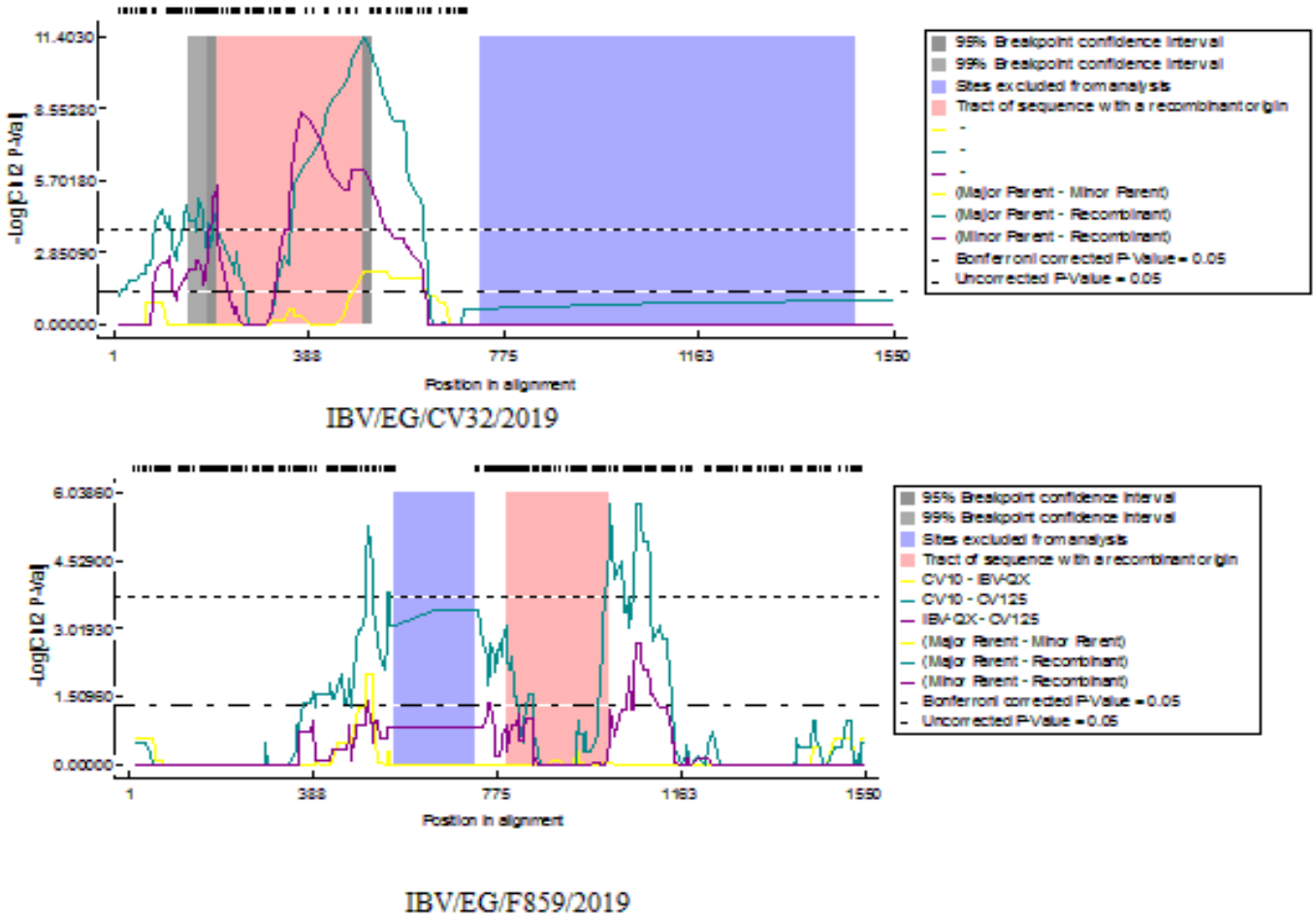

Figure 5. Recombination detection analysis of the S1 gene. Recombination events predicted for IBV/EG/CV32/2019 had a minor recombination from D274 and a major recombination from the Egyptian strain IBV/EG/F859 / 2019. However, the IBV/EG/F859/2019 had a minor recombination of QX and a major one of IBV/EG/CV10/2019.

Recombination analysis

The recombination events of the S1 were detected in two strains, with IBV/EG/CV32 / 2019 indicating a slight recombination from D274 and a larger recombination from the Egyptian strain IBV/EG/F859 / 2019. However, the IBV/EG/F859 / 2019 had a minor recombination of QX and a larger recombination of IBV/EG/CV10 / 2019 (Figure 5). No recombination events were recorded in the nucleotide sequences of the N and M genes.

DISCUSSION

The Infectious bronchitis virus (IBV) is still widespread worldwide and causes massive damage in the poultry industry in both vaccinated and non-vaccinated flocks (Lyb, 2010). Different studies have focused on the epidemiology of the virus (Fathy et al., 2014; Sultanet al., 2019). There is a study emphasizing the hypervariable region of the spike gene (HVR-S) (Abdel-Moneim et al., 2012; Zanaty et al., 2016), but limited genetic information about the major structural protein was reported (S, N, and M). The molecular characterization of S1 and N genes was responsible for the evolutionary analysis of IBV (Lee et al., 2003). Besides, the protein encoded by the S1 and N genes is the most potent antigens for inducing an immune response to IBV infection (Ignjatovic and Galli, 1995). The current study examined the genetic variability and recombination of IBV of the major structural protein (S1, N, and M).

Previous research suggested the genetic classification of IBV based on S1 HVR I (Lee et al., 2003; Zantay et al., 2016), but the findings were not representative due to the presence of multiple mutations throughout the S1 gene detected in the presented study and other previous studies (Schikora et al., 2003; Li et al., 2012). The S1 genes of all strains were clustered in GI-23

(variant II) with three strains clustered into Egy VAR I and the other seven strains clustered in Egy VAR II, as previously reported (Zanaty et al., 2016, Abozeid et al., 2017). However, all of the strains in the present study related to Egy VAR II became a new subgroup.

Multiple outbreaks in the presence of different vaccination programs were previously studied (Abd El Rahman et al., 2015; Sultan et al., 2013). The massive use of classic H120, M41, and variant 4/91 vaccines produced vaccination pressure on the virus leading to the production of a virus escape mutant in the HVR, and accordingly vaccination failure as reported in previous studies (Zanaty et al., 2016; Sultan et al., 2019). Different mutations in the HVRI, II, and III were detected in all strains possibly due to vaccination pressure. Moreover, the currently administered vaccine showed genetically different values as was mentioned before (Rohaim et al., 2019). In this regard, there is a need to conduct further studies to demonstrate the antigenicity ,pathogenicity and the effectiveness of the vaccine of recent field strains.

The N-glycosylation sites in the spike and membrane glycoproteins of IBV had a significant effect on the antigenicity, receptor binding and fusion (Braakman and Van Anken, 2000; Wissink et al., 2004). Variation in N-glycosylation sites could affect receptor interaction, reduce recognition of antibodies leading to a reduction in the innate immune response, and affect the replication and infectivity of the virus (Slater-Handshy et al., 2004; Vigerust and Shepherd, 2007). The difference in the N-glycosylation sites on the spike protein reported in current study requires further studies to show its effect on the pathogenicity of the virus. The N protein played an important role in immunogenicity against IBV infection, and the assembly of viruses (He et al., 2004; You et al., 2007). However, previous studies suggested that the N gene was conserved, which was supported by the detection of all IBV strains (Williams et al., 1992). all strains in this study were divided into a new subgroup with multiple specific mutations as well as the S1 gene with one N-glycosylation site in the N gene, as previously described (Fan et al., 2019). It is therefore required to investigate the effect of this mutation on the immunogenicity and pathogenicity of the virus.

The M protein is responsible for the assembly of virus particle by interactions with other structural proteins (Vennema et al., 1996). The phylogenetic analysis revealed that genotypes based on the S1 gene differ significantly from those of the M gene. There is no differentiation between variant I and II in the characterization of the M gene, as previously described (Shieh et al., 2004; Hughes, 2011). All strain clustered in the variant group with a new subgroup as well as the S1 gene. The rise of multiple new IBV genotypes was observed due to the occurrence of several recombination events within the same genotype or between different genotypes. Others were observed between field and vaccine viruses (Zhang et al., 2010; Han et al., 2016; Jackwood et al., 2010). The recombination was detected in the present study in two isolates from QX and D274 and the same genotype as previously detected in a study conducted by Kiss et al (2016) and no recombination was detected in the N or M gene.

Natural selection usually led to a reduction in harmful mutations, thus promoting beneficial mutations. In general, the gene positively selected by natural selection usually had very important functions (Tang et al., 2009). The positive selection pressure in this study was only detected at five sites in the S1 gene, and was expected due to the extensive use of IBV vaccine as previously described (Jahantigh et al., 2013). This selective pressure could affect the primary and secondary structures of the S1 gene, which led to a change in the genetic and molecular characterization of the virus and the emergence of new strains that, as previously reported, could escape from the immune system (Dolz et al., 2008). Therefore, more research is needed to determine the role of these mutations in the virulence of IBV.

CONCLUSION

The Egyptian IBV has evolved continuously and has acquired special features. The S1 protein is clustered to clad GI23 variant II (the genetic classification of IBV) with three strain clusters into Egy VARI and others cluster to Egy VARII in new subgroup, compared to the previously isolated strain in Egypt with specific mutations, especially in the HVRI, II, and III. The strains included in the study differed significantly from vaccine seeds. The molecular characterization of the M gene and N gene are confirmed as the classification of the S1 gene with a specific feature. The recombination detected in the present study occurred in two isolates from QX and D274. Surveillance of IBV should continue to ensure the early detection of virus mutations and to study the pathogenicity and antigenicity, as well as the evaluation of the vaccine efficacy against newly evolved strains.

DECLERATION

Author`s contribution

Nahed Yehia suggested the title of study and designed the paper, Dalia Said isolated the IBV samples.

Nahed Yehia and Ali Zanaty identified the molecular characterization of isolates. All authors participated in the writing, analysis of the data, and review of the manuscript, and finally approved the last version of manuscript.

Acknowledgement

This study was funded by Animal health research institute.

Competing interests

All authors declared that did not have any conflict of interest.

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Supplementary Table 1. Nucleotide identities and divergence of N gene sequenced viruses compared to other selected strains and vaccine strains. The comparative alignment of N gene showed that the percentage of N AA identity of the tested strain ranged 91- 95% with different vaccine seeds used in Egypt.

Sequence name	IBV/Ck/EG/CU/4/2014	IBV-isolate AR251-15	IBV- 4/91	IBV- CR88121	IBV-serotype Arkansas	IBV/Ck/EG/CU/1/2014,	Avian coronavirus strain Ma5,	IBV-isolate IS/1494	IBV-H120	IBV-EGY/CH/CV10-2019-NP	IBV-EGY/CH/CV17-2019-NP	IBV-EGY/CH/CV31-2019-NP	IBV-EGY/CH/F580-2019-NP	IBV-EGY/CH/CV48-2019-NP	IBV-EGY/CH/CV125-2019-NP	IBV-EGY/CH/F564-2019-NP	IBV-EGY/CH/CV32-2019-NP	IBV-EGY/CH/F742-2019-NP	IBV-EGY/CH/F859-2019-NP
	Nucleotide Identity %																		
1. IBV-IBV/Ck/EG/CU/4/2014		91%	92%	92%	92%	92%	92%	98%	92%	94%	94%	93%	94%	94%	94%	94%	95%	95%	95%
2. IBV-isolate AR251-15	95%		99%	92%	91%	91%	91%	91%	91%	90%	90%	91%	90%	90%	90%	90%	93%	91%	91%
3. IBV- 4/91	96%	99%		93%	92%	92%	92%	92%	92%	91%	91%	91%	91%	91%	91%	91%	93%	91%	91%
4. IBV- CR88121	95%	96%	96%		93%	92%	92%	92%	92%	91%	91%	91%	91%	91%	91%	91%	93%	91%	91%
5. IBV-serotype Arkansas	95%	95%	95%	95%		97%	97%	92%	97%	91%	91%	91%	91%	91%	91%	91%	93%	91%	91%
6. IBV/Ck/EG/CU/1/2014,	94%	95%	96%	94%	98%		100%	93%	100%	91%	91%	91%	91%	91%	91%	91%	93%	91%	91%
7. Avian coronavirus Ma5,	94%	95%	96%	94%	98%	100%		93%	100%	91%	91%	91%	91%	91%	91%	91%	93%	91%	91%
8. IBV-isolate IS/1494	98%	96%	95%	96%	95%	95%	95%		93%	94%	94%	93%	94%	94%	94%	94%	95%	94%	94%
9. IBV-H120	94%	95%	95%	94%	97%	100%	100%	95%		91%	91%	91%	91%	91%	91%	91%	93%	91%	91%
10. IBV-EGY/CH/CV10-2019-NP	96%	93%	93%	94%	92%	92%	92%	96%	91%		100%	99%	100%	100%	100%	100%	96%	99%	99%
11. IBV-EGY/CH/CV17-2019-NP	96%	93%	93%	94%	92%	92%	92%	96%	91%	100%		99%	100%	100%	100%	100%	96%	99%	99%
12. IBV-EGY/CH/CV31-2019-NP	95%	94%	94%	94%	93%	92%	92%	95%	92%	99%	99%		99%	99%	99%	99%	95%	99%	99%
13. IBV-EGY/CH/F580-2019-NP	96%	93%	93%	94%	92%	92%	92%	96%	91%	100%	100%	99%		100%	100%	100%	96%	99%	99%
14. IBV-EGY/CH/CV48-2019-NP	96%	93%	93%	94%	92%	92%	92%	96%	91%	100%	100%	99%	100%		100%	100%	96%	99%	99%
15. IBV-EGY/CH/CV125-2019-NP	96%	93%	93%	94%	92%	92%	92%	96%	91%	100%	100%	99%	100%	100%		100%	96%	99%	99%
16. IBV-EGY/CH/F564-2019-NP	96%	93%	93%	94%	92%	92%	92%	96%	91%	100%	100%	99%	100%	100%	100%		96%	99%	99%
17. IBV-EGY/CH/CV32-2019-NP	97%	95%	95%	95%	94%	94%	94%	97%	94%	97%	97%	97%	97%	97%	97%	97%		96%	96%
18. IBV-EGY/CH/F742-2019-NP	96%	94%	93%	93%	92%	92%	92%	96%	92%	100%	100%	99%	100%	100%	100%	100%	98%		100%
19. IBV-EGY/CH/F859-2019-NP	96%	94%	93%	93%	92%	92%	92%	96%	92%	100%	100%	99%	100%	100%	100%	100%	98%	100%	
	Amino Acids Identity %																		

To cite this paper: Yehia N, Said D and Zanaty AM (2020). Characterization and Analysis of the Major Structural Protein Genes of the Recently Isolated Avian Infectious Bronchitis Virus in Egypt. *J. World Poult. Res.*, 10 (4): 649-661. DOI: https://dx.doi.org/10.36380/jwpr.2020.74

Supplementary table 2. Nucleotide identities and divergence of M gene sequenced viruses compared to other selected strains and vaccine strains. The comparative alignment of M gene showed that the percentage of M gene AA identity of the tested strain ranged 94-96% with different vaccine seeds used in Egypt.

Sequence name	IBV/Ck/EG/CU/4/2014,	IBV-QXIBV-M	IBV/Ck/EG/CU/1/2014	IBV- M41,	IBV-Arkansas Vaccine,	IBV- Conn46 1996,	IBV- 4/91 vaccine,	IBV-AR251-15	IBV-IS/1494/06	IBV-D41	IBV-H120	IBV-EGY/CH/CV32-2019-M	IBV-EGY/CH/CV31-2019-M	IBV-EGY/CH/CV125-2019-M	IBV-EGY/CH/F859-2019-M	IBV-EGY/CH/CV48-2019-M	IBV-EGY/CH/F742-2019-M	IBV-EGY/CH/CV17-2019-M	IBV-EGY/CH/CV10-2019-M	IBV-EGY/CH/F564-2019-M	IBV-EGY/CH/F580-2019-M
Nucleotide Identity %																					
1. IBV/Ck/EG/CU/4/2014,		92%	93%	93%	90%	90%	92%	95%	92%	93%	93%	96%	96%	96%	96%	96%	96%	96%	96%	96%	96%
2. IBV-QXIBV-M	93%		91%	91%	91%	91%	92%	94%	90%	90%	90%	92%	92%	92%	91%	92%	92%	92%	91%	92%	92%
3. IBV/Ck/EG/CU/1/2014	94%	95%		97%	93%	93%	94%	93%	99%	100%	100%	93%	94%	94%	93%	94%	93%	94%	93%	93%	93%
4. IBV- M41,	94%	95%	100%		92%	92%	93%	93%	96%	96%	96%	92%	93%	93%	93%	93%	92%	93%	92%	93%	93%
5. IBV-Arkansas Vaccine,	93%	95%	96%	96%		100%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	91%	92%
6. IBV- Conn46 1996,	93%	95%	96%	96%	100%		92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	92%	91%	92%
7. IBV- 4/91 vaccine,	94%	94%	95%	95%	95%	95%		94%	94%	94%	94%	93%	93%	93%	93%	93%	93%	93%	93%	93%	93%
8. IBV-AR251-15.	95%	94%	95%	95%	95%	95%	95%		93%	93%	93%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%
9. IBV-IS/1494/06	93%	94%	99%	99%	95%	95%	94%	94%		99%	99%	92%	93%	93%	93%	93%	92%	93%	93%	93%	93%
10. IBV-D41	94%	94%	100%	100%	95%	95%	95%	94%	100%		100%	93%	93%	93%	93%	93%	93%	93%	93%	93%	93%
11. IBV-H120	94%	94%	100%	100%	95%	95%	95%	94%	100%	100%		93%	93%	93%	93%	93%	93%	93%	93%	93%	93%
12. IBV-EGY/CH/CV32-2019-M	96%	94%	94%	94%	94%	94%	95%	96%	94%	94%	94%		99%	99%	99%	99%	100%	99%	100%	99%	99%
13. IBV-EGY/CH/CV31-2019-M	96%	94%	95%	95%	94%	94%	96%	96%	94%	94%	94%	100%		100%	100%	100%	99%	100%	99%	100%	100%
14. IBV-EGY/CH/CV125-2019-M	96%	94%	95%	95%	94%	94%	96%	96%	94%	94%	94%	100%	100%		100%	100%	99%	100%	99%	100%	100%
15. IBV-EGY/CH/F859-2019-M	95%	94%	94%	94%	94%	94%	95%	95%	93%	94%	94%	99%	99%	99%		100%	99%	100%	99%	100%	100%
16. IBV-EGY/CH/CV48-2019-M	96%	94%	95%	95%	94%	94%	96%	96%	94%	94%	94%	100%	100%	100%	99%		99%	100%	99%	100%	100%
17. IBV-EGY/CH/F742-2019-M	96%	94%	94%	94%	94%	94%	95%	96%	94%	94%	94%	100%	100%	100%	99%	100%		99%	100%	99%	99%
18. IBV-EGY/CH/CV17-2019-M	96%	94%	95%	95%	94%	94%	96%	96%	94%	94%	94%	100%	100%	100%	99%	100%	99%		99%	100%	100%
19. IBV-EGY/CH/CV10-2019-M	96%	94%	94%	94%	94%	94%	95%	96%	94%	94%	94%	100%	100%	100%	99%	100%	100%	99%		99%	100%
20. IBV-EGY/CH/F564-2019-M	95%	94%	94%	94%	94%	94%	95%	95%	93%	94%	94%	99%	99%	99%	100%	99%	99%	100%	99%		99%
21. IBV-EGY/CH/F580-2019-M	96%	94%	95%	95%	94%	94%	96%	96%	94%	94%	94%	100%	100%	100%	99%	100%	99%	100%	100%	99%	
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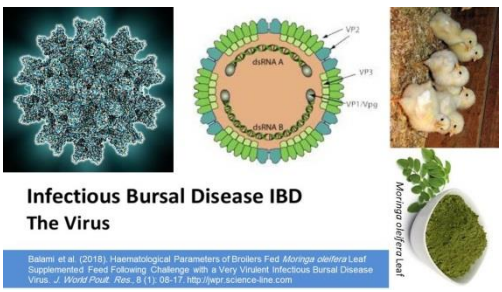

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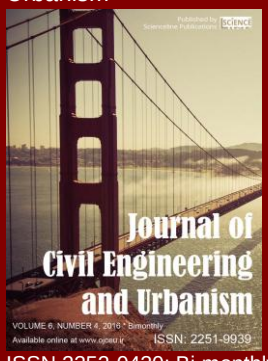

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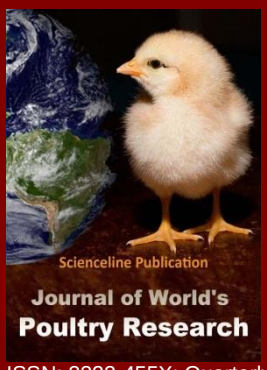

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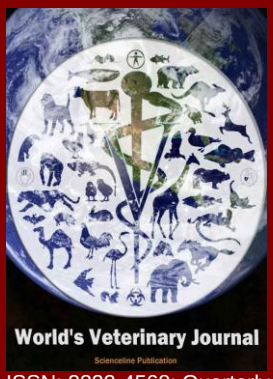

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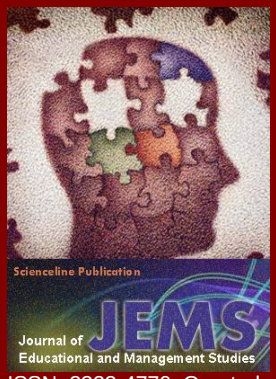

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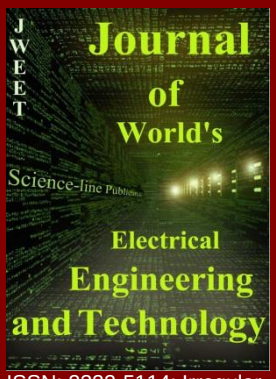

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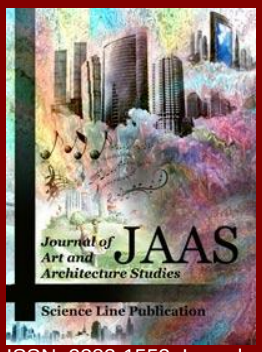

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